GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 5, 2004, 13:18:37 ; Search time 2544 Seconds
(without alignments)
557.662 Million cell updates/sec

Title: US-09-890-363-1
Perfect score: 30
Sequence: 1 gtaattgcggcaagaagaattgtttctgtc 30

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 2024102

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	30	100.0	30	6	BD237979	BD237979 Formulati
	2	30	100.0	30	6	AX032823	AX032823 Sequence
	3	26.8	89.3	30	6	BD237980	BD237980 Formulati
c	4	26.8	89.3	30	6	BD237985	BD237985 Formulati
c	5	26.8	89.3	30	6	BD237989	BD237989 Formulati
	6	26.8	89.3	30	6	AX032824	AX032824 Sequence
c	7	26.8	89.3	30	6	AX032829	AX032829 Sequence
c	8	26.8	89.3	30	6	AX032833	AX032833 Sequence
	9	17.2	57.3	30	6	BD237986	BD237986 Formulati
	10	17.2	57.3	30	6	AX032830	AX032830 Sequence
c	11	17	56.7	43	6	AR411028	AR411028 Sequence
	12	16.8	56.0	65	11	BX547960	BX547960 Arabidops
c	13	16.6	55.3	50	6	AX952037	AX952037 Sequence
c	14	16.6	55.3	50	6	AX952631	AX952631 Sequence
c	15	16.2	54.0	49	6	AX952011	AX952011 Sequence
c	16	16.2	54.0	49	6	AX952044	AX952044 Sequence
c	17	16.2	54.0	49	6	AX952605	AX952605 Sequence
c	18	16.2	54.0	49	6	AX952638	AX952638 Sequence
	19	16.2	54.0	60	6	CQ538369	CQ538369 Sequence
	20	16.2	54.0	70	6	E15744	E15744 DNA encodin
	21	15.8	52.7	41	6	AR109135	AR109135 Sequence
	22	15.8	52.7	41	6	AR200790	AR200790 Sequence
c	23	15.8	52.7	47	6	AR284458	AR284458 Sequence
	24	15.4	51.3	43	6	AX484469	AX484469 Sequence
c	25	15.4	51.3	51	6	CQ007362	CQ007362 Sequence
	26	15.4	51.3	65	6	CQ560587	CQ560587 Sequence
	27	15.2	50.7	40	6	AX774088	AX774088 Sequence
c	28	15	50.0	41	6	AX515819	AX515819 Sequence
c	29	15	50.0	41	6	AX518414	AX518414 Sequence
c	30	15	50.0	50	6	AX952015	AX952015 Sequence
c	31	15	50.0	50	6	AX952045	AX952045 Sequence
c	32	15	50.0	50	6	AX952063	AX952063 Sequence
c	33	15	50.0	50	6	AX952609	AX952609 Sequence
c	34	15	50.0	50	6	AX952639	AX952639 Sequence
c	35	15	50.0	50	6	AX952657	AX952657 Sequence
c	36	15	50.0	60	6	CQ831872	CQ831872 Sequence
	37	14.8	49.3	35	6	E16238	E16238 PCR primer
	38	14.8	49.3	35	6	E16283	E16283 PCR primer
	39	14.8	49.3	35	6	AX128301	AX128301 Sequence
	40	14.8	49.3	36	3	AF251753S5	AF251757 Japyx sp.
c	41	14.8	49.3	43	6	AX484455	AX484455 Sequence
	42	14.8	49.3	47	6	AR284544	AR284544 Sequence
c	43	14.8	49.3	59	6	AX684244	AX684244 Sequence
	44	14.8	49.3	65	6	CQ531914	CQ531914 Sequence
	45	14.8	49.3	65	6	CQ531944	CQ531944 Sequence

ALIGNMENTS

RESULT 1
BD237979
LOCUS BD237979 30 bp DNA linear PAT 17-JUL-2003
DEFINITION Formulations comprising antisense nucleotides to connexins.
ACCESSION BD237979
VERSION BD237979.1 GI:33047749
KEYWORDS JP 2002535377-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Becker,D.L. and Green,C.R.
TITLE Formulations comprising antisense nucleotides to connexins
JOURNAL Patent: JP 2002535377-A 1 22-OCT-2002;
UNIVERSITY COLLEGE LONDON
COMMENT OS Artificial Sequence
PN JP 2002535377-A/1
PD 22-OCT-2002
PF 27-JAN-2000 JP 2000595711
PR 27-JAN-1999 NZ 333928,07-OCT-1999 NZ 500190 PI
DAVID LAURENCE BECKER,COLIN RICHARD GREEN
PC A61K31/711,A61K9/06,A61K9/10,A61K47/16,A61K47/34,A61K47/46, PC A61K48/00,
PC A61P17/02,A61P17/12,A61P17/16,A61P25/00,A61P29/00,A61P43/00,
PC A61P43/00//
PC C12N15/09,C12N15/00
CC Description of Artificial Sequence: Oligonucleotide FH Key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN

Query Match 100.0%; Score 30; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTAATTGCGGCAAGAAGAATTGTTTCTGTC 30

```
              ||||||||||||||||||||||||||||||
Db          1 GTAATTGCGGCAAGAAGAATTGTTTCTGTC 30


RESULT 2
AX032823
LOCUS       AX032823                  30 bp    DNA     linear   PAT 21-SEP-2000
DEFINITION  Sequence 1 from Patent WO0044409.
ACCESSION   AX032823
VERSION     AX032823.1  GI:10279797
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Becker,D.L. and Green,C.R.
  TITLE     Formulations comprising antisense nucleotides to connexins
  JOURNAL   Patent: WO 0044409-A 1 03-AUG-2000;
            BECKER DAVID LAURENCE (GB) ; UNIV LONDON (GB) ; GREEN COLIN RICHARD
            (NZ)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"
ORIGIN

  Query Match             100.0%;  Score 30;  DB 6;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 0.014;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTAATTGCGGCAAGAAGAATTGTTTCTGTC 30
              ||||||||||||||||||||||||||||||
Db          1 GTAATTGCGGCAAGAAGAATTGTTTCTGTC 30


RESULT 3
BD237980
LOCUS       BD237980                  30 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Formulations comprising antisense nucleotides to connexins.
ACCESSION   BD237980
VERSION     BD237980.1  GI:33047750
KEYWORDS    JP 2002535377-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Becker,D.L. and Green,C.R.
  TITLE     Formulations comprising antisense nucleotides to connexins
  JOURNAL   Patent: JP 2002535377-A 2 22-OCT-2002;
            UNIVERSITY COLLEGE LONDON
COMMENT     OS   Artificial Sequence
            PN   JP 2002535377-A/2
            PD   22-OCT-2002
            PF   27-JAN-2000 JP 2000595711
            PR   27-JAN-1999 NZ       333928,07-OCT-1999 NZ       500190 PI
            DAVID LAURENCE BECKER,COLIN RICHARD GREEN
            PC   A61K31/711,A61K9/06,A61K9/10,A61K47/16,A61K47/34,A61K47/46, PC
              A61K48/00,
            PC   A61P17/02,A61P17/12,A61P17/16,A61P25/00,A61P29/00,A61P43/00,
            PC   A61P43/00//
            PC   C12N15/09,C12N15/00
            CC   Description of Artificial Sequence: Oligonucleotide FH   Key
                 Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             89.3%;  Score 26.8;  DB 6;  Length 30;
  Best Local Similarity   93.3%;  Pred. No. 0.39;
  Matches   28;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GTAATTGCGGCAAGAAGAATTGTTTCTGTC 30
              ||||||||||||  || ||||||||||||||
Db          1 GTAATTGCGGCAGGAGGAATTGTTTCTGTC 30


RESULT 4
BD237985/c
LOCUS       BD237985                  30 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Formulations comprising antisense nucleotides to connexins.
ACCESSION   BD237985
VERSION     BD237985.1  GI:33047755
KEYWORDS    JP 2002535377-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Becker,D.L. and Green,C.R.
  TITLE     Formulations comprising antisense nucleotides to connexins
  JOURNAL   Patent: JP 2002535377-A 7 22-OCT-2002;
            UNIVERSITY COLLEGE LONDON
COMMENT     OS   Artificial Sequence
            PN   JP 2002535377-A/7
            PD   22-OCT-2002
            PF   27-JAN-2000 JP 2000595711
            PR   27-JAN-1999 NZ       333928,07-OCT-1999 NZ       500190 PI
            DAVID LAURENCE BECKER,COLIN RICHARD GREEN
            PC   A61K31/711,A61K9/06,A61K9/10,A61K47/16,A61K47/34,A61K47/46, PC
              A61K48/00,
            PC   A61P17/02,A61P17/12,A61P17/16,A61P25/00,A61P29/00,A61P43/00,
            PC   A61P43/00//
            PC   C12N15/09,C12N15/00
            CC   Description of Artificial Sequence: Oligonucleotide FH   Key
                 Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             89.3%;  Score 26.8;  DB 6;  Length 30;
  Best Local Similarity   93.3%;  Pred. No. 0.39;
  Matches   28;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GTAATTGCGGCAAGAAGAATTGTTTCTGTC 30
              ||||||||||||  || ||||||||||||||
Db         30 GTAATTGCGGCAGGAGGAATTGTTTCTGTC 1


RESULT 5
BD237989/c
LOCUS       BD237989                  30 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Formulations comprising antisense nucleotides to connexins.
ACCESSION   BD237989
VERSION     BD237989.1  GI:33047759
KEYWORDS    JP 2002535377-A/11.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Becker,D.L. and Green,C.R.
  TITLE     Formulations comprising antisense nucleotides to connexins
  JOURNAL   Patent: JP 2002535377-A 11 22-OCT-2002;
            UNIVERSITY COLLEGE LONDON
COMMENT     OS   Artificial Sequence
            PN   JP 2002535377-A/11
```

```
            PD   22-OCT-2002
            PF   27-JAN-2000 JP 2000595711
            PR   27-JAN-1999 NZ       333928,07-OCT-1999 NZ       500190 PI
            DAVID LAURENCE BECKER,COLIN RICHARD GREEN
            PC   A61K31/711,A61K9/06,A61K9/10,A61K47/16,A61K47/34,A61K47/46, PC
              A61K48/00,
            PC   A61P17/02,A61P17/12,A61P17/16,A61P25/00,A61P29/00,A61P43/00,
            PC   A61P43/00//
            PC   C12N15/09,C12N15/00
            CC   Description of Artificial Sequence: Oligonucleotide FH   Key
                 Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             89.3%;  Score 26.8;  DB 6;  Length 30;
  Best Local Similarity   93.3%;  Pred. No. 0.39;
  Matches   28;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GTAATTGCGGCAAGAAGAATTGTTTCTGTC 30
              ||||||||||||| || ||||||||||||||
Db         30 GTAATTGCGGCAGGAGGAATTGTTTCTGTC 1


RESULT 6
AX032824
LOCUS       AX032824                  30 bp    DNA     linear   PAT 21-SEP-2000
DEFINITION  Sequence 2 from Patent WO0044409.
ACCESSION   AX032824
VERSION     AX032824.1  GI:10279798
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Becker,D.L. and Green,C.R.
  TITLE     Formulations comprising antisense nucleotides to connexins
  JOURNAL   Patent: WO 0044409-A 2 03-AUG-2000;
            BECKER DAVID LAURENCE (GB) ; UNIV LONDON (GB) ; GREEN COLIN RICHARD
            (NZ)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"
ORIGIN

  Query Match             89.3%;  Score 26.8;  DB 6;  Length 30;
  Best Local Similarity   93.3%;  Pred. No. 0.39;
  Matches   28;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GTAATTGCGGCAAGAAGAATTGTTTCTGTC 30
              ||||||||||||| || ||||||||||||||
Db          1 GTAATTGCGGCAGGAGGAATTGTTTCTGTC 30


RESULT 7
AX032829/c
LOCUS       AX032829                  30 bp    DNA     linear   PAT 21-SEP-2000
DEFINITION  Sequence 7 from Patent WO0044409.
ACCESSION   AX032829
VERSION     AX032829.1  GI:10279803
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Becker,D.L. and Green,C.R.
  TITLE     Formulations comprising antisense nucleotides to connexins
  JOURNAL   Patent: WO 0044409-A 7 03-AUG-2000;
            BECKER DAVID LAURENCE (GB) ; UNIV LONDON (GB) ; GREEN COLIN RICHARD
            (NZ)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"
ORIGIN

  Query Match             89.3%;  Score 26.8;  DB 6;  Length 30;
  Best Local Similarity   93.3%;  Pred. No. 0.39;
  Matches   28;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GTAATTGCGGCAAGAAGAATTGTTTCTGTC 30
              ||||||||||||| || ||||||||||||||
Db         30 GTAATTGCGGCAGGAGGAATTGTTTCTGTC 1


RESULT 8
AX032833/c
LOCUS       AX032833                  30 bp    DNA     linear   PAT 21-SEP-2000
DEFINITION  Sequence 11 from Patent WO0044409.
ACCESSION   AX032833
VERSION     AX032833.1  GI:10279807
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Becker,D.L. and Green,C.R.
  TITLE     Formulations comprising antisense nucleotides to connexins
  JOURNAL   Patent: WO 0044409-A 11 03-AUG-2000;
            BECKER DAVID LAURENCE (GB) ; UNIV LONDON (GB) ; GREEN COLIN RICHARD
            (NZ)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"
ORIGIN

  Query Match             89.3%;  Score 26.8;  DB 6;  Length 30;
  Best Local Similarity   93.3%;  Pred. No. 0.39;
  Matches   28;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GTAATTGCGGCAAGAAGAATTGTTTCTGTC 30
              ||||||||||||| || ||||||||||||||
Db         30 GTAATTGCGGCAGGAGGAATTGTTTCTGTC 1


RESULT 9
BD237986
LOCUS       BD237986                  30 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Formulations comprising antisense nucleotides to connexins.
ACCESSION   BD237986
VERSION     BD237986.1  GI:33047756
KEYWORDS    JP 2002535377-A/8.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Becker,D.L. and Green,C.R.
  TITLE     Formulations comprising antisense nucleotides to connexins
  JOURNAL   Patent: JP 2002535377-A 8 22-OCT-2002;
            UNIVERSITY COLLEGE LONDON
COMMENT     OS   Artificial Sequence
            PN   JP 2002535377-A/8
            PD   22-OCT-2002
```

```
            PF   27-JAN-2000 JP 2000595711
            PR   27-JAN-1999 NZ       333928,07-OCT-1999 NZ       500190 PI
            DAVID LAURENCE BECKER,COLIN RICHARD GREEN
            PC   A61K31/711,A61K9/06,A61K9/10,A61K47/16,A61K47/34,A61K47/46, PC
              A61K48/00,
            PC   A61P17/02,A61P17/12,A61P17/16,A61P25/00,A61P29/00,A61P43/00,
            PC   A61P43/00//
            PC   C12N15/09,C12N15/00
            CC   Description of Artificial Sequence: Oligonucleotide FH   Key
                 Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             57.3%;  Score 17.2;  DB 6;  Length 30;
  Best Local Similarity   73.3%;  Pred. No. 8e+03;
  Matches   22;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 GTAATTGCGGCAAGAAGAATTGTTTCTGTC 30
              ||| || || || || ||||||||   |||
Db          1 GTAGTTACGACAGGAGGAATTGTTCTCGTC 30


RESULT 10
AX032830
LOCUS       AX032830                 30 bp    DNA     linear   PAT 21-SEP-2000
DEFINITION  Sequence 8 from Patent WO0044409.
ACCESSION   AX032830
VERSION     AX032830.1  GI:10279804
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Becker,D.L. and Green,C.R.
  TITLE     Formulations comprising antisense nucleotides to connexins
  JOURNAL   Patent: WO 0044409-A 8 03-AUG-2000;
            BECKER DAVID LAURENCE (GB) ; UNIV LONDON (GB) ; GREEN COLIN RICHARD
            (NZ)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"
ORIGIN

  Query Match             57.3%;  Score 17.2;  DB 6;  Length 30;
  Best Local Similarity   73.3%;  Pred. No. 8e+03;
  Matches   22;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 GTAATTGCGGCAAGAAGAATTGTTTCTGTC 30
              ||| || || || || ||||||||   |||
Db          1 GTAGTTACGACAGGAGGAATTGTTCTCGTC 30


RESULT 11
AR411028/c
LOCUS       AR411028                 43 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 17 from patent US 6635475.
ACCESSION   AR411028
VERSION     AR411028.1  GI:40162606
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   Helmann,J.D.
  TITLE     Bacillus subtilis extracytoplasmic function .sigma. factor
  JOURNAL   Patent: US 6635475-A 17 21-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .43
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             56.7%;  Score 17;  DB 6;  Length 43;
  Best Local Similarity   80.0%;  Pred. No. 1e+04;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 TAATTGCGGCAAGAAGAATTGTTTC 26
              ||  ||| | |||||||| ||||||
Db         31 TACGTGCAGAAAGAAGAAATGTTTC 7


RESULT 12
BX547960
LOCUS       BX547960                 65 bp    DNA     linear   STS 02-JUL-2003
DEFINITION  Arabidopsis thaliana transposon insertion STS SM_3.39244, sequence
            tagged site.
ACCESSION   BX547960
VERSION     BX547960.1  GI:32440780
KEYWORDS    STS; STS, sequence tagged site.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Clarke,J.H., Bowles,B., Carter,J., Hart,D., McCullagh,B., Walsh,S.,
            Langham,S., LeGrys,C., Jones,J.D.G. and Bevan,M.
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 65)
  AUTHORS   Clarke,J.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUL-2003) Clarke J.H., John Innes Centre, Colney
            Lane, Norwich, NR4 7UJ, UK
COMMENT     AT denotes an activation tag dissociation transposon within a
            single line, ET an enhancer trap dissociation transposon, GT a gene
            trap dissociation transposon, MT a mis-expression enhancer trap
            dissociation transposon, SM a defective suppressor mutator
            transposon. _3 denotes a sequence derived from the 3'end of the
            transposon, _5 denotes a sequence derived from the 5'end of the
            transposon BBSRC GARNet, ATIS project
            On-line seed stock requests: http://nasc.nott.ac.uk/ NASC stock
            code: N125955.
FEATURES             Location/Qualifiers
     source          1. .65
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /variety="Columbia-0 NASC stock code N1092"
                     /db_xref="taxon:3702"
                     /clone="AC022520"
                     /note="Derived from superpool 17.29 NASC code N40772"
     STS             1. .65
                     /standard_name="SM_3.39244"
ORIGIN

  Query Match             56.0%;  Score 16.8;  DB 11;  Length 65;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+04;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 ATTGCGGCAAGAAGAATTGT 23
              ||||| |||||||| |||||
Db         19 ATTGCTGCAAGAAGCATTGT 38


RESULT 13
AX952037/c
LOCUS       AX952037                 50 bp    RNA     linear   PAT 08-JAN-2004
DEFINITION  Sequence 94 from Patent WO03093504.
```

```
ACCESSION   AX952037
VERSION     AX952037.1  GI:40782419
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Vater,A., Jarosch,F., Wettich,A. and Klussmann,S.
  TITLE     Method for amplifying nucleic acids
  JOURNAL   Patent: WO 03093504-A 94 13-NOV-2003;
            Noxxon Pharma AG (DE)
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             55.3%;  Score 16.6;  DB 6;  Length 50;
  Best Local Similarity   82.6%;  Pred. No. 1.5e+04;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          8 CGGCAAGAAGAATTGTTTCTGTC 30
              || ||||| |||| |||||| ||
Db         36 CGTCAAGACGAATCGTTTCTTTC 14


RESULT 14
AX952631/c
LOCUS       AX952631                  50 bp    RNA     linear   PAT 08-JAN-2004
DEFINITION  Sequence 186 from Patent WO03093472.
ACCESSION   AX952631
VERSION     AX952631.1  GI:40782971
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Vater,A., Maasch,C., Jarosch,F., Bell,M., Helmling,S.,
            Eschgfaeller,B., Moyroud,E., Stark,S., Klussmann,S., Ruppert,T.,
            Schiene,K., Bahrenberg,G. and Gillen,C.
  TITLE     Cgrp binding nucleic acids
  JOURNAL   Patent: WO 03093472-A 186 13-NOV-2003;
            Gruenenthal GmbH (DE) ; Noxxon Pharma AG (DE)
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="CGRP-binding nucleic acid"
ORIGIN

  Query Match             55.3%;  Score 16.6;  DB 6;  Length 50;
  Best Local Similarity   82.6%;  Pred. No. 1.5e+04;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          8 CGGCAAGAAGAATTGTTTCTGTC 30
              || ||||| |||| |||||| ||
Db         36 CGTCAAGACGAATCGTTTCTTTC 14


RESULT 15
AX952011/c
LOCUS       AX952011                  49 bp    RNA     linear   PAT 08-JAN-2004
DEFINITION  Sequence 68 from Patent WO03093504.
ACCESSION   AX952011
VERSION     AX952011.1  GI:40782393
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Vater,A., Jarosch,F., Wettich,A. and Klussmann,S.
  TITLE     Method for amplifying nucleic acids
  JOURNAL   Patent: WO 03093504-A 68 13-NOV-2003;
            Noxxon Pharma AG (DE)
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             54.0%;  Score 16.2;  DB 6;  Length 49;
  Best Local Similarity   72.4%;  Pred. No. 2.3e+04;
  Matches   21;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          2 TAATTGCGGCAAGAAGAATTGTTTCTGTC 30
              | || |   ||||| |||| |||||| ||
Db         42 TCATCGTCACAAGACGAATCGTTTCTTTC 14


Search completed: November  5, 2004, 16:35:12
Job time : 2550 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 5, 2004, 13:14:14 ; Search time 343 Seconds
(without alignments)
459.133 Million cell updates/sec

Title: US-09-890-363-1
Perfect score: 30
Sequence: 1 gtaattgcggcaagaagaattgtttctgtc 30

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 4224226

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

• Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	30	100.0	30	3	AAA71646	Aaa71646 Connexin
	2	26.8	89.3	30	3	AAA71647	Aaa71647 Connexin
c	3	26.8	89.3	30	3	AAA71652	Aaa71652 Connexin
	4	17.2	57.3	30	3	AAA71653	Aaa71653 Chićken c
c	5	17	56.7	43	10	ADF50888	Adf50888 Bacillus
c	6	16.6	55.3	50	11	ADM73609	Adm73609 CGRP-bind
c	7	16.6	55.3	50	11	ADM68129	Adm68129 Oligonucl
c	8	16.6	55.3	50	11	ADM67851	Adm67851 Rat alpha
c	9	16.2	54.0	49	11	ADM73616	Adm73616 CGRP-bind
c	10	16.2	54.0	49	11	ADM73583	Adm73583 CGRP-bind
c	11	16.2	54.0	49	11	ADM67858	Adm67858 Rat alpha
c	12	16.2	54.0	49	11	ADM68137	Adm68137 Oligonucl
c	13	16.2	54.0	49	11	ADM68170	Adm68170 Oligonucl
c	14	16.2	54.0	49	11	ADM68130	Adm68130 Oligonucl
c	15	16.2	54.0	49	11	ADM67825	Adm67825 Rat alpha
	16	16.2	54.0	60	6	ABN35256	Abn35256 Human spl
	17	16.2	54.0	70	2	AAV23259	Aav23259 Synthetic
	18	15.8	52.7	27	3	AAZ87224	Aaz87224 Pinctada
	19	15.8	52.7	41	2	AAV50625	Aav50625 Brassica
	20	15.8	52.7	41	6	ABL96067	Abl96067 Brassica
	21	15.6	52.0	24	6	ABL41518	Abl41518 Primer #2
	22	15.4	51.3	43	6	ABZ27822	Abz27822 Candida e
c	23	15.4	51.3	51	4	AAL32794	Aal32794 Human SNP
	24	15.4	51.3	65	6	ABN57474	Abn57474 Mouse spl
	25	15.2	50.7	40	10	ACC59609	Acc59609 S aureus
	26	15.2	50.7	57	2	AAQ55412	Aaq55412 Antifunga
c	27	15.2	50.7	73	9	AAL56857	Aal56857 Chimeric
c	28	15.2	50.7	75	2	AAX33550	Aax33550 Rice beta
c	29	15	50.0	50	11	ADM73587	Adm73587 CGRP-bind
c	30	15	50.0	50	11	ADM73635	Adm73635 CGRP-bind
c	31	15	50.0	50	11	ADM73617	Adm73617 CGRP-bind
c	32	15	50.0	50	11	ADM68138	Adm68138 Oligonucl
c	33	15	50.0	50	11	ADM68185	Adm68185 Oligonucl
c	34	15	50.0	50	11	ADM68128	Adm68128 Oligonucl
c	35	15	50.0	50	11	ADM67859	Adm67859 Rat alpha
c	36	15	50.0	50	11	ADM67877	Adm67877 Rat alpha
c	37	15	50.0	50	11	ADM67829	Adm67829 Rat alpha
c	38	15	50.0	50	11	ADM68139	Adm68139 Oligonucl
c	39	15	50.0	50	11	ADM68169	Adm68169 Oligonucl
c	40	15	50.0	60	12	ADQ76911	Adq76911 Escherich
	41	14.8	49.3	29	3	AAA93601	Aaa93601 Human APC
	42	14.8	49.3	34	2	AAX99849	Aax99849 PCR prime
	43	14.8	49.3	35	2	AAV27021	Aav27021 Primer GT
	44	14.8	49.3	35	2	AAV35868	Aav35868 PCR prime
	45	14.8	49.3	35	4	AAS05357	Aas05357 Mouse alp

ALIGNMENTS

RESULT 1
AAA71646
ID AAA71646 standard; DNA; 30 BP.
XX
AC AAA71646;
XX
DT 15-DEC-2000 (first entry)
XX
DE Connexin 43 primer DNA #1.
XX
KW Connexin; connexin 43; cosmetic treatment; therapy; neuroprotective;
KW vulnerary; antiinflammatory; dermatology; site-specific downregulation;
KW neuronal insult; brain; spinal cord; optic nerve; wound healing;
KW inflammation reduction; scar formation; epithelial basal cell division;
KW keratinization; skin rejuvenation; primer; ss.
XX
OS Unidentified.
XX
PN WO200044409-A1.
XX
PD 03-AUG-2000.
XX
PF 27-JAN-2000; 2000WO-GB000238.
XX
PR 27-JAN-1999; 99NZ-00333928.
PR 07-OCT-1999; 99NZ-00500190.
XX
PA (UNLO) UNIV COLLEGE LONDON.
XX
PI Becker DL, Green CR;
XX
DR WPI; 2000-491220/43.
XX
PT New formulation for therapeutic and/or cosmetic treatment of neuronal
PT cell death, inflammation and scar formation, comprises antisense
PT polynucleotide to connexin protein.
XX
PS Claim 9; Page 2; 64pp; English.
XX
CC This invention describes a novel formulation (I) for use in therapeutic
CC and/or cosmetic treatment, comprising at least one antisense
CC polynucleotide (II) to a connexin protein together with a carrier or
CC vehicle. The products of the invention have neuroprotective, vulnerary,
CC antiinflammatory and dermatological activity. (II) is useful in a

CC formulation (I), which is administered to a site on or within a patient
CC for the site-specific downregulation of connexin protein expression. (I)
CC is therefore specifically useful for reducing neuronal cell death
CC resulting from neuronal insult to a specific site in the brain, spinal
CC cord or optic nerve of a patient, for promoting wound healing resulting
CC from trauma, burns or surgery and for reducing inflammation as a result
CC of a wound or physical trauma of the brain, spinal cord or optic nerve
CC and for decreasing scar formation. (I) containing (II) directed to
CC connexin 43 or 31.1 is administered to regulate epithelial basal cell
CC division and growth or to regulate outer layer keratinization,
CC respectively, for skin rejuvenation or thickening for cosmetic or
CC therapeutic purposes (I) downregulates connexin expression in a highly
CC desirable site-specific manner. This sequence represents a connexin-43
CC directed oligonucleotide which is used in the method of the invention
XX
SQ Sequence 30 BP; 8 A; 4 C; 8 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 30; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTAATTGCGGCAAGAAGAATTGTTTCTGTC 30
||||||||||||||||||||||||||||||
Db 1 GTAATTGCGGCAAGAAGAATTGTTTCTGTC 30

RESULT 2
AAA71647
ID AAA71647 standard; DNA; 30 BP.
XX
AC AAA71647;
XX
DT 15-DEC-2000 (first entry)
XX
DE Connexin 43 primer DNA #2.
XX
KW Connexin; connexin 43; cosmetic treatment; therapy; neuroprotective;
KW vulnerary; antiinflammatory; dermatology; site-specific downregulation;
KW neuronal insult; brain; spinal cord; optic nerve; wound healing;
KW inflammation reduction; scar formation; epithelial basal cell division;
KW keratinization; skin rejuvenation; primer; ss.
XX
OS Unidentified.
XX
PN WO200044409-A1.
XX
PD 03-AUG-2000.
XX
PF 27-JAN-2000; 2000WO-GB000238.
XX
PR 27-JAN-1999; 99NZ-00333928.
PR 07-OCT-1999; 99NZ-00500190.
XX
PA (UNLO) UNIV COLLEGE LONDON.
XX
PI Becker DL, Green CR;
XX
DR WPI; 2000-491220/43.
XX
PT New formulation for therapeutic and/or cosmetic treatment of neuronal
PT cell death, inflammation and scar formation, comprises antisense
PT polynucleotide to connexin protein.
XX
PS Claim 9; Page 2; 64pp; English.
XX
CC This invention describes a novel formulation (I) for use in therapeutic
CC and/or cosmetic treatment, comprising at least one antisense
CC polynucleotide (II) to a connexin protein together with a carrier or
CC vehicle. The products of the invention have neuroprotective, vulnerary,
CC antiinflammatory and dermatological activity. (II) is useful in a
CC formulation (I), which is administered to a site on or within a patient
CC for the site-specific downregulation of connexin protein expression. (I)
CC is therefore specifically useful for reducing neuronal cell death
CC resulting from neuronal insult to a specific site in the brain, spinal
CC cord or optic nerve of a patient, for promoting wound healing resulting
CC from trauma, burns or surgery and for reducing inflammation as a result
CC of a wound or physical trauma of the brain, spinal cord or optic nerve
CC and for decreasing scar formation. (I) containing (II) directed to
CC connexin 43 or 31.1 is administered to regulate epithelial basal cell
CC division and growth or to regulate outer layer keratinization,
CC respectively, for skin rejuvenation or thickening for cosmetic or
CC therapeutic purposes (I) downregulates connexin expression in a highly
CC desirable site-specific manner. This sequence represents a connexin-43
CC directed oligonucleotide which is used in the method of the invention
XX
SQ Sequence 30 BP; 6 A; 4 C; 10 G; 10 T; 0 U; 0 Other;

Query Match 89.3%; Score 26.8; DB 3; Length 30;
Best Local Similarity 93.3%; Pred. No. 0.054;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTAATTGCGGCAAGAAGAATTGTTTCTGTC 30
|||||||||||| || ||||||||||||||
Db 1 GTAATTGCGGCAGGAGGAATTGTTTCTGTC 30

RESULT 3
AAA71652/c
ID AAA71652 standard; DNA; 30 BP.
XX
AC AAA71652;
XX
DT 15-DEC-2000 (first entry)
XX
DE Connexin 43 primer DB1sense DNA.
XX
KW Connexin; connexin 43; cosmetic treatment; therapy; neuroprotective;
KW vulnerary; antiinflammatory; dermatology; site-specific downregulation;
KW neuronal insult; brain; spinal cord; optic nerve; wound healing;
KW inflammation reduction; scar formation; epithelial basal cell division;
KW keratinization; skin rejuvenation; primer; ss.
XX
OS Unidentified.
XX
PN WO200044409-A1.
XX
PD 03-AUG-2000.
XX
PF 27-JAN-2000; 2000WO-GB000238.
XX
PR 27-JAN-1999; 99NZ-00333928.
PR 07-OCT-1999; 99NZ-00500190.
XX
PA (UNLO) UNIV COLLEGE LONDON.
XX
PI Becker DL, Green CR;
XX
DR WPI; 2000-491220/43.
XX
PT New formulation for therapeutic and/or cosmetic treatment of neuronal
PT cell death, inflammation and scar formation, comprises antisense
PT polynucleotide to connexin protein.
XX
PS Example 1; Page 17; 64pp; English.
XX
CC This invention describes a novel formulation (I) for use in therapeutic
CC and/or cosmetic treatment, comprising at least one antisense
CC polynucleotide (II) to a connexin protein together with a carrier or
CC vehicle. The products of the invention have neuroprotective, vulnerary,
CC antiinflammatory and dermatological activity. (II) is useful in a
CC formulation (I), which is administered to a site on or within a patient
CC for the site-specific downregulation of connexin protein expression. (I)
CC is therefore specifically useful for reducing neuronal cell death
CC resulting from neuronal insult to a specific site in the brain, spinal
CC cord or optic nerve of a patient, for promoting wound healing resulting
CC from trauma, burns or surgery and for reducing inflammation as a result

```
CC   of a wound or physical trauma of the brain, spinal cord or optic nerve
CC   and for decreasing scar formation. (I) containing (II) directed to
CC   connexin 43 or 31.1 is administered to regulate epithelial basal cell
CC   division and growth or to regulate outer layer keratinization,
CC   respectively, for skin rejuvenation or thickening for cosmetic or
CC   therapeutic purposes (I) downregulates connexin expression in a highly
CC   desirable site-specific manner. This sequence represents a connexin-43
CC   directed oligonucleotide which is used in the method of the invention
XX
SQ   Sequence 30 BP; 10 A; 10 C; 4 G; 6 T; 0 U; 0 Other;

  Query Match             89.3%;  Score 26.8;  DB 3;  Length 30;
  Best Local Similarity   93.3%;  Pred. No. 0.054;
  Matches   28;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GTAATTGCGGCAAGAAGAATTGTTTCTGTC 30
              |||||||||||| || ||||||||||||||
Db         30 GTAATTGCGGCAGGAGGAATTGTTTCTGTC 1


RESULT 4
AAA71653
ID   AAA71653 standard; DNA; 30 BP.
XX
AC   AAA71653;
XX
DT   15-DEC-2000  (first entry)
XX
DE   Chicken connexin 43 primer DB1 DNA.
XX
KW   Connexin; connexin 43; cosmetic treatment; therapy; neuroprotective;
KW   vulnerary; antiinflammatory; dermatology; site-specific downregulation;
KW   neuronal insult; brain; spinal cord; optic nerve; wound healing;
KW   inflammation reduction; scar formation; epithelial basal cell division;
KW   keratinization; skin rejuvenation; primer; chicken; ss.
XX
OS   Gallus sp.
XX
PN   WO200044409-A1.
XX
PD   03-AUG-2000.
XX
PF   27-JAN-2000; 2000WO-GB000238.
XX
PR   27-JAN-1999;   99NZ-00333928.
PR   07-OCT-1999;   99NZ-00500190.
XX
PA   (UNLO ) UNIV COLLEGE LONDON.
XX
PI   Becker DL,  Green CR;
XX
DR   WPI; 2000-491220/43.
XX
PT   New formulation for therapeutic and/or cosmetic treatment of neuronal
PT   cell death, inflammation and scar formation, comprises antisense
PT   polynucleotide to connexin protein.
XX
PS   Example 1; Page 17; 64pp; English.
XX
CC   This invention describes a novel formulation (I) for use in therapeutic
CC   and/or cosmetic treatment, comprising at least one antisense
CC   polynucleotide (II) to a connexin protein together with a carrier or
CC   vehicle. The products of the invention have neuroprotective, vulnerary,
CC   antiinflammatory and dermatological activity. (II) is useful in a
CC   formulation (I), which is administered to a site on or within a patient
CC   for the site-specific downregulation of connexin protein expression. (I)
CC   is therefore specifically useful for reducing neuronal cell death
CC   resulting from neuronal insult to a specific site in the brain, spinal
CC   cord or optic nerve of a patient, for promoting wound healing resulting
CC   from trauma, burns or surgery and for reducing inflammation as a result
CC   of a wound or physical trauma of the brain, spinal cord or optic nerve
CC   and for decreasing scar formation. (I) containing (II) directed to
CC   connexin 43 or 31.1 is administered to regulate epithelial basal cell
CC   division and growth or to regulate outer layer keratinization,
CC   respectively, for skin rejuvenation or thickening for cosmetic or
CC   therapeutic purposes (I) downregulates connexin expression in a highly
CC   desirable site-specific manner. This sequence represents a connexin-43
CC   directed oligonucleotide which is used in the method of the invention
XX
SQ   Sequence 30 BP; 7 A; 5 C; 9 G; 9 T; 0 U; 0 Other;

  Query Match             57.3%;  Score 17.2;  DB 3;  Length 30;
  Best Local Similarity   73.3%;  Pred. No. 9.1e+02;
  Matches   22;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 GTAATTGCGGCAAGAAGAATTGTTTCTGTC 30
              ||| || || || || ||||||||   |||
Db          1 GTAGTTACGACAGGAGGAATTGTTCTCGTC 30


RESULT 5
ADF50888/c
ID   ADF50888 standard; DNA; 43 BP.
XX
AC   ADF50888;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Bacillus subtilis yfhL DNA oligo homologous to sigW.
XX
KW   ss; ECF; sigma factor; extracytoplasmic function;
KW   autoregulatory promoter; Px; sigW; Pw; detoxification; antimicrobial;
KW   bacterial growth; replication; sigX.
XX
OS   Bacillus subtilis.
XX
PN   US6635475-B1.
XX
PD   21-OCT-2003.
XX
PF   28-JUL-2000; 2000US-00627746.
XX
PR   30-JUL-1999;   99US-0146466P.
XX
PA   (CORR ) CORNELL RES FOUND INC.
XX
PI   Helmann JD;
XX
DR   WPI; 2003-810568/76.
XX
PT   New Bacillus subtilis sigW gene encoding an extracytoplasmic function
PT   alpha factor, useful for screening assays to identify potential
PT   antibacterial agents.
XX
PS   Disclosure; SEQ ID NO 17; 18pp; English.
XX
CC   This invention relates to novel Bacillus subtilis extracytoplasmic
CC   function (ECF) sigma factors. These ECF sigma factors regulate their own
CC   expression, accordingly the sigX operon is preceded by an autoregulatory
CC   promoter named Px and likewise the sigW operon is autoregualted by the W-
CC   dependent promoter Pw. A consensus based search approach was used to
CC   identify further operons preceded by promoters similar in sequence to Pw
CC   and hence recognised by SigW, such that SigW has been shown to control a
CC   regulon of more than 30 genes including flotillin and epoxide hydrolase.
CC   Specifically, SigW activates a large stationary phase regulon that
CC   functions in detoxification and/ or the production of antimicrobial
CC   compounds that can be used to modulate bacterial growth and replication.
CC   This oligonucleotide sequence is the Bacillus subtilis yfhL DNA that is
CC   homologous to sigW of the invention.
XX
SQ   Sequence 43 BP; 14 A; 8 C; 8 G; 13 T; 0 U; 0 Other;

  Query Match             56.7%;  Score 17;  DB 10;  Length 43;
  Best Local Similarity   80.0%;  Pred. No. 1.2e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;
```

```
Qy          2 TAATTGCGGCAAGAAGAATTGTTTC 26
              ||  ||| | ||||||||  ||||||
Db         31 TACGTGCAGAAAGAAGAAATGTTTC 7
```

RESULT 6
ADM73609/c
ID ADM73609 standard; RNA; 50 BP.
XX
AC ADM73609;
XX
DT 03-JUN-2004 (first entry)
XX
DE CGRP-binding ribo-oligonucleotide STAR-R02-15d-G12.
XX
KW antagonist; CGRP; calcitonin gene-related peptide; amylin; amyloid;
KW spiegelmer; migraine; cluster headache; appetite loss; nausea; vomiting;
KW neurogenic inflammation; vasodilation; hypotension; hypertension;
KW tachycardia; trigeminal afferent sensory neuron activation;
KW central nociceptive neuron; inflammatory pain; diabetes;
KW gastric emptying; diabetic gastroparesis; polydypsia; ss.
XX
OS Synthetic.
XX
PN WO2003093472-A2.
XX
PD 13-NOV-2003.
XX
PF 06-MAY-2003; 2003WO-EP004746.
XX
PR 06-MAY-2002; 2002DE-01020188.
PR 04-NOV-2002; 2002DE-01051246.
XX
PA (CHEF) GRUENENTHAL GMBH.
PA (NOXX-) NOXXON PHARMA AG.
XX
PI Vater A, Maasch C, Jarosch F, Bell M, Helmling S, Eschgfaeller B;
PI Moyroud E, Stark S, Klussmann S, Ruppert T, Schiene K, Bahrenberg G;
PI Gillen C;
XX
DR WPI; 2003-854484/79.
XX
PT New antagonists of calcitonin gene-related peptide or amylin, useful for
PT treating or preventing e.g. migraine or inflammation, are specific
PT binding nucleic acids.
XX
PS Claim 15; SEQ ID NO 186; 263pp; German.
XX
CC This invention describes a novel antagonist of CGRP (calcitonin gene-
CC related peptide), amylin or an amyloid polypeptide. A library of RNA (2'-
CC fluoro substituted on pyrimidine nucleotides) was incubated with
CC biotinylated CGRP, for 3 hours at 37degC, then the incubation mixture
CC applied to a matrix coated with streptavidin for 10 minutes at 37degC.
CC The matrix was separated, washed with selection buffer and bound RNA
CC recovered by elution with an excess of non-biotinylated CGRP. The bound
CC RNA released this way was amplified and the selection procedure repeated
CC for a total of 18 rounds, after which reverse transcription produced 192
CC clones. One sequence was present in 168 of these clones. This sequence
CC had a Kd of 10 nM and was used as starting sequence for preparation of
CC optimised and truncated RNA aptamers or spiegelmers (RTM). Antagonists of
CC CGRP, amylin and amyloid polypeptides are useful for treating and/or
CC preventing: migraine, cluster headache, lack of appetite, nausea,
CC vomiting, neurogenic inflammation (especially where mediated by other
CC neuropeptides), vasodilation, hypo- or hyper-tension, tachycardia,
CC diseases that are associated with activation of trigeminal afferent
CC sensory neurons and central nociceptive neurons (especially of the higher
CC pain centres and including chronic inflammatory pain) and/or pain
CC generally (chronic, acute, inflammatory, visceral or neuropathic), where
CC CGRP is the target and hypertension, diabetes, disorders of gastric
CC emptying, diabetic gastroparesis and polydypsia, where amylin or amyloid
CC peptides are the target. Antagonists that are nucleic acids are also
CC useful for detecting CGRP, amylin and amyloid polypeptides or plaques, to
CC screen for other CGRP and amylin antagonists or agonists, as starting
CC materials for rational drug design, for target validation and for
CC studying CGRP or amylin function.
XX
SQ Sequence 50 BP; 16 A; 9 C; 16 G; 0 T; 9 U; 0 Other;

Query Match 55.3%; Score 16.6; DB 11; Length 50;
Best Local Similarity 82.6%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          8 CGGCAAGAAGAATTGTTTCTGTC 30
              || ||||| |||| |||||| ||
Db         36 CGTCAAGACGAATCGTTTCTTTC 14
```

RESULT 7
ADM68129/c
ID ADM68129 standard; DNA; 50 BP.
XX
AC ADM68129;
XX
DT 03-JUN-2004 (first entry)
XX
DE Oligonucleotide STAR-R02-15d-G12.
XX
KW nucleic acid amplification; antimigraine; analgesic; L-nucleic acid;
KW CGRP antagonist; calcitonin gene-related peptide; amylin; pain;
KW drug design; primer; ss.
XX
OS Synthetic.
XX
PN WO2003093504-A1.
XX
PD 13-NOV-2003.
XX
PF 06-MAY-2003; 2003WO-EP004747.
XX
PR 06-MAY-2002; 2002DE-01020191.
XX
PA (NOXX-) NOXXON PHARMA AG.
XX
PI Vater A, Jarosch F, Wettich A, Klussmann S;
XX
DR WPI; 2003-854487/79.
XX
PT Amplification of nucleic acid using two adapters, useful for selection
PT and preparation of aptamers, potential therapeutic agents, with all steps
PT done in one vessel.
XX
PS Example 12; Fig 35; 262pp; German.
XX
CC This invention describes a novel method for amplifying nucleic acids. The
CC method comprises 1) preparing a target to be amplified, preferably RNA,
CC having defined 5' and 3' sequences, separated by an intermediate
CC sequence, 2) preparing a first adapter (Ad1) of double-stranded nucleic
CC acid (especially one strand of RNA and the other DNA), where the 5'-end
CC of the DNA strand has an overhang at least partly complementary with the
CC 5'-end of the target, 3) preparing a second adapter (Ad2) of double
CC stranded nucleic acid, where the first strand has a 5'-phosphate residue
CC on (deoxy)ribose and the second strand (DNA) has a 3'-end that is at
CC least partly complementary with the 3'-end of the target, the second
CC strand also has a cleavage site which can generate a cleavage product
CC that includes the complementary 3'-end of the second strand, 4) the
CC adapters are ligated on the target, 5) reverse transcription is performed
CC and optionally the second strand is synthesised. The products of the
CC invention have antimigraine and analgesic activity. The method is
CC especially used for selection and preparation of nucleic acids including
CC L-nucleic acids, that bind to selected targets (aptamers), potentially
CC useful as therapeutic agents, e.g. as antagonists of CGRP (calcitonin
CC gene-related peptide) or amylin or their receptors, suitable for
CC treatment of pain, migraine and other conditions, also as starting points
CC for rational drug design, in screening for therapeutic compounds and for
CC target validation. The method can be done in a single vessel, without
CC purification of process intermediates and it can be applied to short

CC sequences.
XX
SQ Sequence 50 BP; 16 A; 9 C; 16 G; 9 T; 0 U; 0 Other;

Query Match 55.3%; Score 16.6; DB 11; Length 50;
Best Local Similarity 82.6%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          8 CGGCAAGAAGAATTGTTTCTGTC 30
              || ||||| |||| |||||| ||
Db         36 CGTCAAGACGAATCGTTTCTTTC 14
```

RESULT 8
ADM67851/c
ID ADM67851 standard; RNA; 50 BP.
XX
AC ADM67851;
XX
DT 03-JUN-2004 (first entry)
XX
DE Rat alpha-D-CGRP binding oligonucleotide SEQ ID 94.
XX
KW nucleic acid amplification; antimigraine; analgesic; L-nucleic acid;
KW CGRP antagonist; calcitonin gene-related peptide; amylin; pain;
KW drug design; primer; ss.
XX
OS Rattus sp.
XX
PN WO2003093504-A1.
XX
PD 13-NOV-2003.
XX
PF 06-MAY-2003; 2003WO-EP004747.
XX
PR 06-MAY-2002; 2002DE-01020191.
XX
PA (NOXX-) NOXXON PHARMA AG.
XX
PI Vater A, Jarosch F, Wettich A, Klussmann S;
XX
DR WPI; 2003-854487/79.
XX
PT Amplification of nucleic acid using two adapters, useful for selection
PT and preparation of aptamers, potential therapeutic agents, with all steps
PT done in one vessel.
XX
PS Example 12; SEQ ID NO 94; 262pp; German.
XX
CC This invention describes a novel method for amplifying nucleic acids. The
CC method comprises 1) preparing a target to be amplified, preferably RNA,
CC having defined 5' and 3' sequences, separated by an intermediate
CC sequence, 2) preparing a first adapter (Ad1) of double-stranded nucleic
CC acid (especially one strand of RNA and the other DNA), where the 5'-end
CC of the DNA strand has an overhang at least partly complementary with the
CC 5'-end of the target, 3) preparing a second adapter (Ad2) of double
CC stranded nucleic acid, where the first strand has a 5'-phosphate residue
CC on (deoxy)ribose and the second strand (DNA) has a 3'-end that is at
CC least partly complementary with the 3'-end of the target, the second
CC strand also has a cleavage site which can generate a cleavage product
CC that includes the complementary 3'-end of the second strand, 4) the
CC adapters are ligated on the target, 5) reverse transcription is performed
CC and optionally the second strand is synthesised. The products of the
CC invention have antimigraine and analgesic activity. The method is
CC especially used for selection and preparation of nucleic acids including
CC L-nucleic acids, that bind to selected targets (aptamers), potentially
CC useful as therapeutic agents, e.g. as antagonists of CGRP (calcitonin
CC gene-related peptide) or amylin or their receptors, suitable for
CC treatment of pain, migraine and other conditions, also as starting points
CC for rational drug design, in screening for therapeutic compounds and for
CC target validation. The method can be done in a single vessel, without
CC purification of process intermediates and it can be applied to short
CC sequences. ADM67759-ADM67903 represent oligoribonucleotides capable of
CC binding to rat CGRP which are used to illustrate the method of the
CC invention.
XX
SQ Sequence 50 BP; 16 A; 9 C; 16 G; 0 T; 9 U; 0 Other;

Query Match 55.3%; Score 16.6; DB 11; Length 50;
Best Local Similarity 82.6%; Pred. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          8 CGGCAAGAAGAATTGTTTCTGTC 30
              || ||||| |||| |||||| ||
Db         36 CGTCAAGACGAATCGTTTCTTTC 14
```

RESULT 9
ADM73616/c
ID ADM73616 standard; RNA; 49 BP.
XX
AC ADM73616;
XX
DT 03-JUN-2004 (first entry)
XX
DE CGRP-binding ribo-oligonucleotide STAR-R02-15xx-B10.
XX
KW antagonist; CGRP; calcitonin gene-related peptide; amylin; amyloid;
KW spiegelmer; migraine; cluster headache; appetite loss; nausea; vomiting;
KW neurogenic inflammation; vasodilation; hypotension; hypertension;
KW tachycardia; trigeminal afferent sensory neuron activation;
KW central nociceptive neuron; inflammatory pain; diabetes;
KW gastric emptying; diabetic gastroparesis; polydypsia; ss.
XX
OS Synthetic.
XX
PN WO2003093472-A2.
XX
PD 13-NOV-2003.
XX
PF 06-MAY-2003; 2003WO-EP004746.
XX
PR 06-MAY-2002; 2002DE-01020188.
PR 04-NOV-2002; 2002DE-01051246.
XX
PA (CHEF) GRUENENTHAL GMBH.
PA (NOXX-) NOXXON PHARMA AG.
XX
PI Vater A, Maasch C, Jarosch F, Bell M, Helmling S, Eschgfaeller B;
PI Moyroud E, Stark S, Klussmann S, Ruppert T, Schiene K, Bahrenberg G;
PI Gillen C;
XX
DR WPI; 2003-854484/79.
XX
PT New antagonists of calcitonin gene-related peptide or amylin, useful for
PT treating or preventing e.g. migraine or inflammation, are specific
PT binding nucleic acids.
XX
PS Claim 15; SEQ ID NO 193; 263pp; German.
XX
CC This invention describes a novel antagonist of CGRP (calcitonin gene-
CC related peptide), amylin or an amyloid polypeptide. A library of RNA (2'-
CC fluoro substituted on pyrimidine nucleotides) was incubated with
CC biotinylated CGRP, for 3 hours at 37degC, then the incubation mixture
CC applied to a matrix coated with streptavidin for 10 minutes at 37degC.
CC The matrix was separated, washed with selection buffer and bound RNA
CC recovered by elution with an excess of non-biotinylated CGRP. The bound
CC RNA released this way was amplified and the selection procedure repeated
CC for a total of 18 rounds, after which reverse transcription produced 192
CC clones. One sequence was present in 168 of these clones. This sequence
CC had a Kd of 10 nM and was used as starting sequence for preparation of
CC optimised and truncated RNA aptamers or spiegelmers (RTM). Antagonists of
CC CGRP, amylin and amyloid polypeptides are useful for treating and/or
CC preventing: migraine, cluster headache, lack of appetite, nausea,
CC vomiting, neurogenic inflammation (especially where mediated by other
CC neuropeptides), vasodilation, hypo- or hyper-tension, tachycardia,

CC diseases that are associated with activation of trigeminal afferent
CC sensory neurons and central nociceptive neurons (especially of the higher
CC pain centres and including chronic inflammatory pain) and/or pain
CC generally (chronic, acute, inflammatory, visceral or neuropathic), where
CC CGRP is the target and hypertension, diabetes, disorders of gastric
CC emptying, diabetic gastroparesis and polydypsia, where amylin or amyloid
CC peptides are the target. Antagonists that are nucleic acids are also
CC useful for detecting CGRP, amylin and amyloid polypeptides or plaques, to
CC screen for other CGRP and amylin antagonists or agonists, as starting
CC materials for rational drug design, for target validation and for
CC studying CGRP or amylin function.
XX
SQ Sequence 49 BP; 16 A; 9 C; 16 G; 0 T; 8 U; 0 Other;

Query Match 54.0%; Score 16.2; DB 11; Length 49;
Best Local Similarity 72.4%; Pred. No. 2.7e+03;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 TAATTGCGGCAAGAAGAATTGTTTCTGTC 30
Db 42 TCATCGTCGCTAGACGAATCGTTTCTTTC 14

RESULT 10
ADM73583/c
ID ADM73583 standard; RNA; 49 BP.
XX
AC ADM73583;
XX
DT 03-JUN-2004 (first entry)
XX
DE CGRP-binding ribo-oligonucleotide STAR-R02-12MW-E3.
XX
KW antagonist; CGRP; calcitonin gene-related peptide; amylin; amyloid;
KW spiegelmer; migraine; cluster headache; appetite loss; nausea; vomiting;
KW neurogenic inflammation; vasodilation; hypotension; hypertension;
KW tachycardia; trigeminal afferent sensory neuron activation;
KW central nociceptive neuron; inflammatory pain; diabetes;
KW gastric emptying; diabetic gastroparesis; polydypsia; ss.
XX
OS Synthetic.
XX
PN WO2003093472-A2.
XX
PD 13-NOV-2003.
XX
PF 06-MAY-2003; 2003WO-EP004746.
XX
PR 06-MAY-2002; 2002DE-01020188.
PR 04-NOV-2002; 2002DE-01051246.
XX
PA (CHEF) GRUENENTHAL GMBH.
PA (NOXX-) NOXXON PHARMA AG.
XX
PI Vater A, Maasch C, Jarosch F, Bell M, Helmling S, Eschgfaeller B;
PI Moyroud E, Stark S, Klussmann S, Ruppert T, Schiene K, Bahrenberg G;
PI Gillen C;
XX
DR WPI; 2003-854484/79.
XX
PT New antagonists of calcitonin gene-related peptide or amylin, useful for
PT treating or preventing e.g. migraine or inflammation, are specific
PT binding nucleic acids.
XX
PS Claim 15; SEQ ID NO 160; 263pp; German.
XX
CC This invention describes a novel antagonist of CGRP (calcitonin gene-
CC related peptide), amylin or an amyloid polypeptide. A library of RNA (2'-
CC fluoro substituted on pyrimidine nucleotides) was incubated with
CC biotinylated CGRP, for 3 hours at 37degC, then the incubation mixture
CC applied to a matrix coated with streptavidin for 10 minutes at 37degC.
CC The matrix was separated, washed with selection buffer and bound RNA
CC recovered by elution with an excess of non-biotinylated CGRP. The bound
CC RNA released this way was amplified and the selection procedure repeated
CC for a total of 18 rounds, after which reverse transcription produced 192
CC clones. One sequence was present in 168 of these clones. This sequence
CC had a Kd of 10 nM and was used as starting sequence for preparation of
CC optimised and truncated RNA aptamers or spiegelmers (RTM). Antagonists of
CC CGRP, amylin and amyloid polypeptides are useful for treating and/or
CC preventing: migraine, cluster headache, lack of appetite, nausea,
CC vomiting, neurogenic inflammation (especially where mediated by other
CC neuropeptides), vasodilation, hypo- or hyper-tension, tachycardia,
CC diseases that are associated with activation of trigeminal afferent
CC sensory neurons and central nociceptive neurons (especially of the higher
CC pain centres and including chronic inflammatory pain) and/or pain
CC generally (chronic, acute, inflammatory, visceral or neuropathic), where
CC CGRP is the target and hypertension, diabetes, disorders of gastric
CC emptying, diabetic gastroparesis and polydypsia, where amylin or amyloid
CC peptides are the target. Antagonists that are nucleic acids are also
CC useful for detecting CGRP, amylin and amyloid polypeptides or plaques, to
CC screen for other CGRP and amylin antagonists or agonists, as starting
CC materials for rational drug design, for target validation and for
CC studying CGRP or amylin function.
XX
SQ Sequence 49 BP; 15 A; 8 C; 16 G; 0 T; 10 U; 0 Other;

Query Match 54.0%; Score 16.2; DB 11; Length 49;
Best Local Similarity 72.4%; Pred. No. 2.7e+03;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 TAATTGCGGCAAGAAGAATTGTTTCTGTC 30
Db 42 TCATCGTCACAAGACGAATCGTTTCTTTC 14

RESULT 11
ADM67858/c
ID ADM67858 standard; RNA; 49 BP.
XX
AC ADM67858;
XX
DT 03-JUN-2004 (first entry)
XX
DE Rat alpha-D-CGRP binding oligonucleotide SEQ ID 101.
XX
KW nucleic acid amplification; antimigraine; analgesic; L-nucleic acid;
KW CGRP antagonist; calcitonin gene-related peptide; amylin; pain;
KW drug design; primer; ss.
XX
OS Rattus sp.
XX
PN WO2003093504-A1.
XX
PD 13-NOV-2003.
XX
PF 06-MAY-2003; 2003WO-EP004747.
XX
PR 06-MAY-2002; 2002DE-01020191.
XX
PA (NOXX-) NOXXON PHARMA AG.
XX
PI Vater A, Jarosch F, Wettich A, Klussmann S;
XX
DR WPI; 2003-854487/79.
XX
PT Amplification of nucleic acid using two adapters, useful for selection
PT and preparation of aptamers, potential therapeutic agents, with all steps
PT done in one vessel.
XX
PS Example 12; SEQ ID NO 101; 262pp; German.
XX
CC This invention describes a novel method for amplifying nucleic acids. The
CC method comprises 1) preparing a target to be amplified, preferably RNA,
CC having defined 5' and 3' sequences, separated by an intermediate
CC sequence, 2) preparing a first adapter (Ad1) of double-stranded nucleic
CC acid (especially one strand of RNA and the other DNA), where the 5'-end

CC of the DNA strand has an overhang at least partly complementary with the
CC 5'-end of the target, 3) preparing a second adapter (Ad2) of double
CC stranded nucleic acid, where the first strand has a 5'-phosphate residue
CC on (deoxy)ribose and the second strand (DNA) has a 3'-end that is at
CC least partly complementary with the 3'-end of the target, the second
CC strand also has a cleavage site which can generate a cleavage product
CC that includes the complementary 3'-end of the second strand, 4) the
CC adapters are ligated on the target, 5) reverse transcription is performed
CC and optionally the second strand is synthesised. The products of the
CC invention have antimigraine and analgesic activity. The method is
CC especially used for selection and preparation of nucleic acids including
CC L-nucleic acids, that bind to selected targets (aptamers), potentially
CC useful as therapeutic agents, e.g. as antagonists of CGRP (calcitonin
CC gene-related peptide) or amylin or their receptors, suitable for
CC treatment of pain, migraine and other conditions, also as starting points
CC for rational drug design, in screening for therapeutic compounds and for
CC target validation. The method can be done in a single vessel, without
CC purification of process intermediates and it can be applied to short
CC sequences. ADM67759-ADM67903 represent oligoribonucleotides capable of
CC binding to rat CGRP which are used to illustrate the method of the
CC invention.
XX
SQ Sequence 49 BP; 16 A; 9 C; 16 G; 0 T; 8 U; 0 Other;

Query Match 54.0%; Score 16.2; DB 11; Length 49;
Best Local Similarity 72.4%; Pred. No. 2.7e+03;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 TAATTGCGGCAAGAAGAATTGTTTCTGTC 30
| || | || ||| |||| |||||| ||
Db 42 TCATCGTCGCTAGACGAATCGTTTCTTTC 14

RESULT 12
ADM68137/c
ID ADM68137 standard; DNA; 49 BP.
XX
AC ADM68137;
XX
DT 03-JUN-2004 (first entry)
XX
DE Oligonucleotide STAR-R02-12MW-E3.
XX
KW nucleic acid amplification; antimigraine; analgesic; L-nucleic acid;
KW CGRP antagonist; calcitonin gene-related peptide; amylin; pain;
KW drug design; primer; ss.
XX
OS Synthetic.
XX
PN WO2003093504-A1.
XX
PD 13-NOV-2003.
XX
PF 06-MAY-2003; 2003WO-EP004747.
XX
PR 06-MAY-2002; 2002DE-01020191.
XX
PA (NOXX-) NOXXON PHARMA AG.
XX
PI Vater A, Jarosch F, Wettich A, Klussmann S;
XX
DR WPI; 2003-854487/79.
XX
PT Amplification of nucleic acid using two adapters, useful for selection
PT and preparation of aptamers, potential therapeutic agents, with all steps
PT done in one vessel.
XX
PS Example 12; Fig 36; 262pp; German.
XX
CC This invention describes a novel method for amplifying nucleic acids. The
CC method comprises 1) preparing a target to be amplified, preferably RNA,
CC having defined 5' and 3' sequences, separated by an intermediate
CC sequence, 2) preparing a first adapter (Ad1) of double-stranded nucleic
CC acid (especially one strand of RNA and the other DNA), where the 5'-end
CC of the DNA strand has an overhang at least partly complementary with the
CC 5'-end of the target, 3) preparing a second adapter (Ad2) of double
CC stranded nucleic acid, where the first strand has a 5'-phosphate residue
CC on (deoxy)ribose and the second strand (DNA) has a 3'-end that is at
CC least partly complementary with the 3'-end of the target, the second
CC strand also has a cleavage site which can generate a cleavage product
CC that includes the complementary 3'-end of the second strand, 4) the
CC adapters are ligated on the target, 5) reverse transcription is performed
CC and optionally the second strand is synthesised. The products of the
CC invention have antimigraine and analgesic activity. The method is
CC especially used for selection and preparation of nucleic acids including
CC L-nucleic acids, that bind to selected targets (aptamers), potentially
CC useful as therapeutic agents, e.g. as antagonists of CGRP (calcitonin
CC gene-related peptide) or amylin or their receptors, suitable for
CC treatment of pain, migraine and other conditions, also as starting points
CC for rational drug design, in screening for therapeutic compounds and for
CC target validation. The method can be done in a single vessel, without
CC purification of process intermediates and it can be applied to short
CC sequences.
XX
SQ Sequence 49 BP; 15 A; 8 C; 16 G; 10 T; 0 U; 0 Other;

Query Match 54.0%; Score 16.2; DB 11; Length 49;
Best Local Similarity 72.4%; Pred. No. 2.7e+03;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 TAATTGCGGCAAGAAGAATTGTTTCTGTC 30
| || | |||| |||| |||||| ||
Db 42 TCATCGTCACAAGACGAATCGTTTCTTTC 14

RESULT 13
ADM68170/c
ID ADM68170 standard; DNA; 49 BP.
XX
AC ADM68170;
XX
DT 03-JUN-2004 (first entry)
XX
DE Oligonucleotide STAR-R02-15xx-B10.
XX
KW nucleic acid amplification; antimigraine; analgesic; L-nucleic acid;
KW CGRP antagonist; calcitonin gene-related peptide; amylin; pain;
KW drug design; primer; ss.
XX
OS Synthetic.
XX
PN WO2003093504-A1.
XX
PD 13-NOV-2003.
XX
PF 06-MAY-2003; 2003WO-EP004747.
XX
PR 06-MAY-2002; 2002DE-01020191.
XX
PA (NOXX-) NOXXON PHARMA AG.
XX
PI Vater A, Jarosch F, Wettich A, Klussmann S;
XX
DR WPI; 2003-854487/79.
XX
PT Amplification of nucleic acid using two adapters, useful for selection
PT and preparation of aptamers, potential therapeutic agents, with all steps
PT done in one vessel.
XX
PS Example 12; Fig 37; 262pp; German.
XX
CC This invention describes a novel method for amplifying nucleic acids. The
CC method comprises 1) preparing a target to be amplified, preferably RNA,
CC having defined 5' and 3' sequences, separated by an intermediate
CC sequence, 2) preparing a first adapter (Ad1) of double-stranded nucleic
CC acid (especially one strand of RNA and the other DNA), where the 5'-end

CC of the DNA strand has an overhang at least partly complementary with the
CC 5'-end of the target, 3) preparing a second adapter (Ad2) of double
CC stranded nucleic acid, where the first strand has a 5'-phosphate residue
CC on (deoxy)ribose and the second strand (DNA) has a 3'-end that is at
CC least partly complementary with the 3'-end of the target, the second
CC strand also has a cleavage site which can generate a cleavage product
CC that includes the complementary 3'-end of the second strand, 4) the
CC adapters are ligated on the target, 5) reverse transcription is performed
CC and optionally the second strand is synthesised. The products of the
CC invention have antimigraine and analgesic activity. The method is
CC especially used for selection and preparation of nucleic acids including
CC L-nucleic acids, that bind to selected targets (aptamers), potentially
CC useful as therapeutic agents, e.g. as antagonists of CGRP (calcitonin
CC gene-related peptide) or amylin or their receptors, suitable for
CC treatment of pain, migraine and other conditions, also as starting points
CC for rational drug design, in screening for therapeutic compounds and for
CC target validation. The method can be done in a single vessel, without
CC purification of process intermediates and it can be applied to short
CC sequences.
XX
SQ Sequence 49 BP; 16 A; 9 C; 16 G; 8 T; 0 U; 0 Other;

Query Match 54.0%; Score 16.2; DB 11; Length 49;
Best Local Similarity 72.4%; Pred. No. 2.7e+03;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 TAATTGCGGCAAGAAGAATTGTTTCTGTC 30
| || | || ||| |||| |||||| ||
Db 42 TCATCGTCGCTAGACGAATCGTTTCTTTC 14

RESULT 14
ADM68130/c
ID ADM68130 standard; DNA; 49 BP.
XX
AC ADM68130;
XX
DT 03-JUN-2004 (first entry)
XX
DE Oligonucleotide STAR-R02-15d-E1.
XX
KW nucleic acid amplification; antimigraine; analgesic; L-nucleic acid;
KW CGRP antagonist; calcitonin gene-related peptide; amylin; pain;
KW drug design; primer; ss.
XX
OS Synthetic.
XX
PN WO2003093504-A1.
XX
PD 13-NOV-2003.
XX
PF 06-MAY-2003; 2003WO-EP004747.
XX
PR 06-MAY-2002; 2002DE-01020191.
XX
PA (NOXX-) NOXXON PHARMA AG.
XX
PI Vater A, Jarosch F, Wettich A, Klussmann S;
XX
DR WPI; 2003-854487/79.
XX
PT Amplification of nucleic acid using two adapters, useful for selection
PT and preparation of aptamers, potential therapeutic agents, with all steps
PT done in one vessel.
XX
PS Example 12; Fig 35; 262pp; German.
XX
CC This invention describes a novel method for amplifying nucleic acids. The
CC method comprises 1) preparing a target to be amplified, preferably RNA,
CC having defined 5' and 3' sequences, separated by an intermediate
CC sequence, 2) preparing a first adapter (Ad1) of double-stranded nucleic
CC acid (especially one strand of RNA and the other DNA), where the 5'-end
CC of the DNA strand has an overhang at least partly complementary with the
CC 5'-end of the target, 3) preparing a second adapter (Ad2) of double
CC stranded nucleic acid, where the first strand has a 5'-phosphate residue
CC on (deoxy)ribose and the second strand (DNA) has a 3'-end that is at
CC least partly complementary with the 3'-end of the target, the second
CC strand also has a cleavage site which can generate a cleavage product
CC that includes the complementary 3'-end of the second strand, 4) the
CC adapters are ligated on the target, 5) reverse transcription is performed
CC and optionally the second strand is synthesised. The products of the
CC invention have antimigraine and analgesic activity. The method is
CC especially used for selection and preparation of nucleic acids including
CC L-nucleic acids, that bind to selected targets (aptamers), potentially
CC useful as therapeutic agents, e.g. as antagonists of CGRP (calcitonin
CC gene-related peptide) or amylin or their receptors, suitable for
CC treatment of pain, migraine and other conditions, also as starting points
CC for rational drug design, in screening for therapeutic compounds and for
CC target validation. The method can be done in a single vessel, without
CC purification of process intermediates and it can be applied to short
CC sequences.
XX
SQ Sequence 49 BP; 16 A; 9 C; 16 G; 8 T; 0 U; 0 Other;

Query Match 54.0%; Score 16.2; DB 11; Length 49;
Best Local Similarity 72.4%; Pred. No. 2.7e+03;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 TAATTGCGGCAAGAAGAATTGTTTCTGTC 30
| || | || ||| |||| |||||| ||
Db 42 TCATCGTCGCTAGACGAATCGTTTCTTTC 14

RESULT 15
ADM67825/c
ID ADM67825 standard; RNA; 49 BP.
XX
AC ADM67825;
XX
DT 03-JUN-2004 (first entry)
XX
DE Rat alpha-D-CGRP binding oligonucleotide SEQ ID 68.
XX
KW nucleic acid amplification; antimigraine; analgesic; L-nucleic acid;
KW CGRP antagonist; calcitonin gene-related peptide; amylin; pain;
KW drug design; primer; ss.
XX
OS Rattus sp.
XX
PN WO2003093504-A1.
XX
PD 13-NOV-2003.
XX
PF 06-MAY-2003; 2003WO-EP004747.
XX
PR 06-MAY-2002; 2002DE-01020191.
XX
PA (NOXX-) NOXXON PHARMA AG.
XX
PI Vater A, Jarosch F, Wettich A, Klussmann S;
XX
DR WPI; 2003-854487/79.
XX
PT Amplification of nucleic acid using two adapters, useful for selection
PT and preparation of aptamers, potential therapeutic agents, with all steps
PT done in one vessel.
XX
PS Example 12; SEQ ID NO 68; 262pp; German.
XX
CC This invention describes a novel method for amplifying nucleic acids. The
CC method comprises 1) preparing a target to be amplified, preferably RNA,
CC having defined 5' and 3' sequences, separated by an intermediate
CC sequence, 2) preparing a first adapter (Ad1) of double-stranded nucleic
CC acid (especially one strand of RNA and the other DNA), where the 5'-end
CC of the DNA strand has an overhang at least partly complementary with the
CC 5'-end of the target, 3) preparing a second adapter (Ad2) of double

CC stranded nucleic acid, where the first strand has a 5'-phosphate residue
CC on (deoxy)ribose and the second strand (DNA) has a 3'-end that is at
CC least partly complementary with the 3'-end of the target, the second
CC strand also has a cleavage site which can generate a cleavage product
CC that includes the complementary 3'-end of the second strand, 4) the
CC adapters are ligated on the target, 5) reverse transcription is performed
CC and optionally the second strand is synthesised. The products of the
CC invention have antimigraine and analgesic activity. The method is
CC especially used for selection and preparation of nucleic acids including
CC L-nucleic acids, that bind to selected targets (aptamers), potentially
CC useful as therapeutic agents, e.g. as antagonists of CGRP (calcitonin
CC gene-related peptide) or amylin or their receptors, suitable for
CC treatment of pain, migraine and other conditions, also as starting points
CC for rational drug design, in screening for therapeutic compounds and for
CC target validation. The method can be done in a single vessel, without
CC purification of process intermediates and it can be applied to short
CC sequences. ADM67759-ADM67903 represent oligoribonucleotides capable of
CC binding to rat CGRP which are used to illustrate the method of the
CC invention.
XX
SQ Sequence 49 BP; 15 A; 8 C; 16 G; 0 T; 10 U; 0 Other;

Query Match 54.0%; Score 16.2; DB 11; Length 49;
Best Local Similarity 72.4%; Pred. No. 2.7e+03;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```
Qy          2 TAATTGCGGCAAGAAGAATTGTTTCTGTC 30
              | || |   ||||| |||| |||||| ||
Db         42 TCATCGTCACAAGACGAATCGTTTCTTTC 14
```

Search completed: November 5, 2004, 15:52:39
Job time : 347 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 5, 2004, 15:29:37 ; Search time 71 Seconds
(without alignments)
300.333 Million cell updates/sec

Title: US-09-890-363-1
Perfect score: 30
Sequence: 1 gtaattgcggcaagaagaattgtttctgtc 30

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 983458

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	17	56.7	43	4	US-09-627-746-17	Sequence 17, Appl
	2	15.8	52.7	41	3	US-08-813-507-94	Sequence 94, Appl
	3	15.8	52.7	41	3	US-09-464-453-94	Sequence 94, Appl
c	4	15.8	52.7	47	4	US-09-671-317-510	Sequence 510, App
c	5	15.2	50.7	75	3	US-09-105-390-25	Sequence 25, Appl
	6	14.8	49.3	47	4	US-09-671-317-596	Sequence 596, App
c	7	14.8	49.3	73	1	US-08-434-001-42	Sequence 42, Appl
c	8	14.8	49.3	73	1	US-08-433-585-42	Sequence 42, Appl
c	9	14.8	49.3	73	1	US-08-434-425-42	Sequence 42, Appl
c	10	14.8	49.3	73	2	US-08-437-667-42	Sequence 42, Appl
c	11	14.8	49.3	73	3	US-08-906-955-42	Sequence 42, Appl
c	12	14.8	49.3	73	3	US-08-945-909-42	Sequence 42, Appl
c	13	14.8	49.3	73	3	US-09-396-002A-42	Sequence 42, Appl
c	14	14.8	49.3	73	4	US-10-077-319-42	Sequence 42, Appl
c	15	14.8	49.3	73	5	PCT-US96-06060-42	Sequence 42, Appl
	16	14.6	48.7	40	1	US-07-741-940-14	Sequence 14, Appl
	17	14.6	48.7	40	1	US-08-289-548A-14	Sequence 14, Appl
	18	14.6	48.7	40	1	US-08-452-654-14	Sequence 14, Appl
	19	14.6	48.7	40	1	US-08-452-655B-14	Sequence 14, Appl
	20	14.6	48.7	40	3	US-08-450-582-14	Sequence 14, Appl
	21	14.6	48.7	40	4	US-08-449-731-14	Sequence 14, Appl
	22	14.4	48.0	57	4	US-09-270-767-29842	Sequence 29842, A
	23	14.4	48.0	61	3	US-09-275-850-56	Sequence 56, Appl
c	24	14.2	47.3	27	3	US-09-257-584-13	Sequence 13, Appl
c	25	14	46.7	24	3	US-09-186-170-15	Sequence 15, Appl
c	26	14	46.7	24	4	US-09-562-868-15	Sequence 15, Appl
c	27	14	46.7	24	4	US-10-116-288-15	Sequence 15, Appl
c	28	14	46.7	27	3	US-09-186-170-16	Sequence 16, Appl
c	29	14	46.7	27	4	US-09-562-868-16	Sequence 16, Appl
c	30	14	46.7	27	4	US-10-116-288-16	Sequence 16, Appl
c	31	14	46.7	30	3	US-09-186-170-17	Sequence 17, Appl
c	32	14	46.7	30	4	US-09-562-868-17	Sequence 17, Appl
c	33	14	46.7	30	4	US-10-116-288-17	Sequence 17, Appl
c	34	14	46.7	33	3	US-09-186-170-14	Sequence 14, Appl
c	35	14	46.7	33	3	US-09-186-170-18	Sequence 18, Appl
c	36	14	46.7	33	4	US-09-562-868-14	Sequence 14, Appl
c	37	14	46.7	33	4	US-09-562-868-18	Sequence 18, Appl
c	38	14	46.7	33	4	US-10-116-288-14	Sequence 14, Appl
c	39	14	46.7	33	4	US-10-116-288-18	Sequence 18, Appl
c	40	14	46.7	36	3	US-09-186-170-10	Sequence 10, Appl
c	41	14	46.7	36	4	US-09-562-868-10	Sequence 10, Appl
c	42	14	46.7	36	4	US-10-116-288-10	Sequence 10, Appl
	43	14	46.7	47	4	US-09-380-190A-32	Sequence 32, Appl
c	44	13.8	46.0	20	4	US-09-198-452A-3644	Sequence 3644, Ap
	45	13.8	46.0	23	4	US-09-502-240-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-09-627-746-17/c
; Sequence 17, Application US/09627746
; Patent No. 6635475
; GENERAL INFORMATION:
; APPLICANT: Helmann, John
; TITLE OF INVENTION: Bacillus subtilis Extracytoplasmic Function Sigma Factor
; FILE REFERENCE: 10845-125
; CURRENT APPLICATION NUMBER: US/09/627,746
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/146,466
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 43
; TYPE: DNA
; ORGANISM: Bacillus subtilis
US-09-627-746-17

Query Match 56.7%; Score 17; DB 4; Length 43;
Best Local Similarity 80.0%; Pred. No. 97;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy          2 TAATTGCGGCAAGAAGAATTGTTTC 26
              ||  ||| | |||||||| ||||||
Db         31 TACGTGCAGAAAGAAGAAATGTTTC 7
```

RESULT 2
US-08-813-507-94
; Sequence 94, Application US/08813507
; Patent No. 6114116
; GENERAL INFORMATION:
; APPLICANT: Lemieux, Bertrand
; APPLICANT: Landry, Benoit S.
; APPLICANT: Sapolsky, Ronald J.
; TITLE OF INVENTION: Brassica Polymorphisms
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

```
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/813,507
;      FILING DATE:  07-MAR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/032,069
;      FILING DATE:  02-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Liebeschuetz, Joe
;      REGISTRATION NUMBER:  37,505
;      REFERENCE/DOCKET NUMBER:  018547-030100US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415 576-0200
;      TELEFAX:  415 576-0200
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  94:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  41 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-813-507-94

  Query Match             52.7%;  Score 15.8;  DB 3;  Length 41;
  Best Local Similarity   74.1%;  Pred. No. 3.4e+02;
  Matches   20;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          4 ATTGCGGCAAGAAGAATTGTTTCTGTC 30
              |||| | |  || | ||||||||| ||
Db         12 ATTGGGTCTTGATGGATTGTTTCTATC 38


RESULT 3
US-09-464-453-94
; Sequence 94, Application US/09464453
; Patent No. 6358686
;   GENERAL INFORMATION:
;        APPLICANT: Lemieux, Bertrand
;                   Landry, Benoit S.
;                   Sapolsky, Ronald J.
;        TITLE OF INVENTION: Brassica Polymorphisms
;        NUMBER OF SEQUENCES: 173
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/464,453
;             FILING DATE: 14-Dec-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/813,507
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Liebeschuetz, Joe
;             REGISTRATION NUMBER: 37,505
;             REFERENCE/DOCKET NUMBER: 018547-030100US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415 576-0200
;             TELEFAX: 415 576-0200
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 94:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 41 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 94:
US-09-464-453-94

  Query Match             52.7%;  Score 15.8;  DB 3;  Length 41;
  Best Local Similarity   74.1%;  Pred. No. 3.4e+02;
  Matches   20;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          4 ATTGCGGCAAGAAGAATTGTTTCTGTC 30
              |||| | |  || | ||||||||| ||
Db         12 ATTGGGTCTTGATGGATTGTTTCTATC 38


RESULT 4
US-09-671-317-510/c
; Sequence 510, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Cohen, Annick
;  TITLE OF INVENTION:  BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
;  FILE REFERENCE:  62.US3.CIP
;  CURRENT APPLICATION NUMBER: US/09/671,317
;  CURRENT FILING DATE:  2000-09-27
;  PRIOR APPLICATION NUMBER:  US 09/536,178
;  PRIOR FILING DATE:  2000-03-23
;  PRIOR APPLICATION NUMBER:  PCT/IB00/00403
;  PRIOR FILING DATE:  2000-03-24
;  PRIOR APPLICATION NUMBER:  US 60/126,269
;  PRIOR FILING DATE:  1999-03-25
;  PRIOR APPLICATION NUMBER:  US 60/131,961
;  PRIOR FILING DATE:  1999-04-30
;  NUMBER OF SEQ ID NOS:  977
;  SOFTWARE:  Patent.pm
; SEQ ID NO 510
;   LENGTH: 47
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 24
;   OTHER INFORMATION: 12-456-269 : polymorphic base A or G
US-09-671-317-510

  Query Match             52.7%;  Score 15.8;  DB 4;  Length 47;
  Best Local Similarity   74.1%;  Pred. No. 3.5e+02;
  Matches   20;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          3 AATTGCGGCAAGAAGAATTGTTTCTGT 29
              |||| | || |||||||||  | || |
Db         30 AATTCCYGCTAGAAGAATTCCTGCTCT 4


RESULT 5
US-09-105-390-25/c
; Sequence 25, Application US/09105390
; Patent No. 6288303
;  GENERAL INFORMATION:
;    APPLICANT:  Rodriguez, Raymond
;    TITLE OF INVENTION:  Rice Beta-Glucanase Enzymes
;    TITLE OF INVENTION:  and Genes
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Ave., Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
```

```
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/105,390
;      FILING DATE:  Filed herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/050,675
;      FILING DATE:  25-JUN-97
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Petithory, Joanne R.
;      REGISTRATION NUMBER:  P42,995
;      REFERENCE/DOCKET NUMBER:  2000-0455.30
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-324-0880
;      TELEFAX:  650-324-0960
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  75 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...75
;      OTHER INFORMATION:
US-09-105-390-25

  Query Match             50.7%;  Score 15.2;  DB 3;  Length 75;
  Best Local Similarity   71.4%;  Pred. No. 7.2e+02;
  Matches   20;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 GTAATTGCGGCAAGAAGAATTGTTTCTG 28
              | || ||| ||||| || | || | |||
Db         59 GGAAATGCTGCAAGGAGCAATGCTACTG 32


RESULT 6
US-09-671-317-596
; Sequence 596, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Cohen, Annick
;  TITLE OF INVENTION:  BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
;  FILE REFERENCE:  62.US3.CIP
;  CURRENT APPLICATION NUMBER: US/09/671,317
;  CURRENT FILING DATE:  2000-09-27
;  PRIOR APPLICATION NUMBER:  US 09/536,178
;  PRIOR FILING DATE:  2000-03-23
;  PRIOR APPLICATION NUMBER:  PCT/IB00/00403
;  PRIOR FILING DATE:  2000-03-24
;  PRIOR APPLICATION NUMBER:  US 60/126,269
;  PRIOR FILING DATE:  1999-03-25
;  PRIOR APPLICATION NUMBER:  US 60/131,961
;  PRIOR FILING DATE:  1999-04-30
;  NUMBER OF SEQ ID NOS:  977
;  SOFTWARE:  Patent.pm
; SEQ ID NO 596
;  LENGTH: 47
;  TYPE: DNA
;  ORGANISM: Homo Sapiens
;  FEATURE:
;  NAME/KEY: allele
;  LOCATION: 24
;  OTHER INFORMATION: 2-11-284 : polymorphic base A or G
US-09-671-317-596

  Query Match             49.3%;  Score 14.8;  DB 4;  Length 47;
  Best Local Similarity   80.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         11 CAAGAAGAATTGTTTCTGTC 30
              ||||:||| |||| ||| ||
Db         20 CAAGRAGATTTGTGTCTATC 39


RESULT 7
US-08-434-001-42/c
; Sequence 42, Application US/08434001
; Patent No. 5712375
;  GENERAL INFORMATION:
;    APPLICANT:  JENSEN, KIRK
;    APPLICANT:  CHEN, HANG
;    APPLICANT:  MORRIS, KEVIN
;    APPLICANT:  STEPHENS, ANDREW
;    APPLICANT:  GOLD, LARRY
;    TITLE OF INVENTION:  SYSTEMATIC EVOLUTION OF LIGANDS BY
;    TITLE OF INVENTION:  EXPONENTIAL ENRICYMENT:  TISSUE
;    TITLE OF INVENTION:  SELEX
;    NUMBER OF SEQUENCES:  235
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Swanson & Bratschun, L.L.C.
;      STREET:  8400 E. Prentice Avenue, Suite 200
;      CITY:  Englewood
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3 1/2 diskette, 1.44 MB
;      COMPUTER:  IBM pc compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/434,001
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/714,131
;      FILING DATE:  10-JUNE-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/536,428
;      FILING DATE:  11-JUNE-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/964,624
;      FILING DATE:  21-OCTOBER-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Barry J. Swanson
;      REGISTRATION NUMBER:  33,215
;      REFERENCE/DOCKET NUMBER:  NEX30.3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 793-3333
;      TELEFAX:  (303) 793-3433
;  INFORMATION FOR SEQ ID NO:  42:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  73 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-434-001-42

  Query Match             49.3%;  Score 14.8;  DB 1;  Length 73;
  Best Local Similarity   73.1%;  Pred. No. 1.1e+03;
  Matches   19;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          3 AATTGCGGCAAGAAGAATTGTTTCTG 28
              ||| || |||||||  |  |||||
Db         55 AATAGCAGCAAGAAATAGGGTTTCGG 30
```

```
RESULT 8
US-08-433-585-42/c
; Sequence 42, Application US/08433585
; Patent No. 5763566
;  GENERAL INFORMATION:
;    APPLICANT:  JENSEN, KIRK
;    APPLICANT:  CHEN, HANG
;    APPLICANT:  MORRIS, KEVIN
;    APPLICANT:  STEPHENS, ANDREW
;    APPLICANT:  GOLD, LARRY
;    TITLE OF INVENTION:  SYSTEMATIC EVOLUTION OF LIGANDS BY
;    TITLE OF INVENTION:  EXPONENTIAL ENRICYMENT:  TISSUE
;    TITLE OF INVENTION:  SELEX
;    NUMBER OF SEQUENCES:  235
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Swanson & Bratschun, L.L.C.
;      STREET:  8400 E. Prentice Avenue, Suite 200
;      CITY:  Englewood
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3 1/2 diskette, 1.44 MB
;      COMPUTER:  IBM pc compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/433,585
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/714,131
;      FILING DATE:  10-JUNE-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/536,428
;      FILING DATE:  11-JUNE-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/964,624
;      FILING DATE:  21-OCTOBER-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Barry J. Swanson
;      REGISTRATION NUMBER:  33,215
;      REFERENCE/DOCKET NUMBER:  NEX30.4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 793-3333
;      TELEFAX:  (303) 793-3433
;  INFORMATION FOR SEQ ID NO:  42:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  73 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-433-585-42

  Query Match             49.3%;  Score 14.8;  DB 1;  Length 73;
  Best Local Similarity   73.1%;  Pred. No. 1.1e+03;
  Matches   19;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          3 AATTGCGGCAAGAAGAATTGTTTCTG 28
              ||| || |||||||  |  ||||| |
Db         55 AATAGCAGCAAGAAATAGGGTTTCGG 30


RESULT 9
US-08-434-425-42/c
; Sequence 42, Application US/08434425
; Patent No. 5789157
;  GENERAL INFORMATION:
;    APPLICANT:  JENSEN, KIRK
;    APPLICANT:  CHEN, HANG
;    APPLICANT:  MORRIS, KEVIN
;    APPLICANT:  STEPHENS, ANDREW
;    APPLICANT:  GOLD, LARRY
;    TITLE OF INVENTION:  SYSTEMATIC EVOLUTION OF LIGANDS BY
;    TITLE OF INVENTION:  EXPONENTIAL ENRICYMENT:  TISSUE
;    TITLE OF INVENTION:  SELEX
;    NUMBER OF SEQUENCES:  235
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Swanson & Bratschun, L.L.C.
;      STREET:  8400 E. Prentice Avenue, Suite 200
;      CITY:  Englewood
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3 1/2 diskette, 1.44 MB
;      COMPUTER:  IBM pc compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/434,425
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/714,131
;      FILING DATE:  10-JUNE-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/536,428
;      FILING DATE:  11-JUNE-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/964,624
;      FILING DATE:  21-OCTOBER-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Barry J. Swanson
;      REGISTRATION NUMBER:  33,215
;      REFERENCE/DOCKET NUMBER:  NEX30.1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 793-3333
;      TELEFAX:  (303) 793-3433
;  INFORMATION FOR SEQ ID NO:  42:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  73 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-434-425-42

  Query Match             49.3%;  Score 14.8;  DB 1;  Length 73;
  Best Local Similarity   73.1%;  Pred. No. 1.1e+03;
  Matches   19;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          3 AATTGCGGCAAGAAGAATTGTTTCTG 28
              ||| || |||||||  |  ||||| |
Db         55 AATAGCAGCAAGAAATAGGGTTTCGG 30


RESULT 10
US-08-437-667-42/c
; Sequence 42, Application US/08437667
; Patent No. 5864026
;  GENERAL INFORMATION:
;    APPLICANT:  JENSEN, KIRK
;    APPLICANT:  CHEN, HANG
;    APPLICANT:  MORRIS, KEVIN
;    APPLICANT:  STEPHENS, ANDREW
;    APPLICANT:  GOLD, LARRY
;    TITLE OF INVENTION:  SYSTEMATIC EVOLUTION OF LIGANDS BY
;    TITLE OF INVENTION:  EXPONENTIAL ENRICYMENT:  TISSUE
;    TITLE OF INVENTION:  SELEX
;    NUMBER OF SEQUENCES:  235
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Swanson & Bratschun, L.L.C.
;      STREET:  8400 E. Prentice Avenue, Suite 200
;      CITY:  Englewood
;      STATE:  Colorado
;      COUNTRY:  USA
```

```
;       ZIP:  80111
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette, 3 1/2 diskette, 1.44 MB
;       COMPUTER:  IBM pc compatible
;       OPERATING SYSTEM:  MS-DOS
;       SOFTWARE:  WordPerfect 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/437,667
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/714,131
;       FILING DATE:  10-JUNE-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/536,428
;       FILING DATE:  11-JUNE-1990
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/964,624
;       FILING DATE:  21-OCTOBER-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Barry J. Swanson
;       REGISTRATION NUMBER:  33,215
;       REFERENCE/DOCKET NUMBER:  NEX30.2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (303) 793-3333
;       TELEFAX:  (303) 793-3433
;   INFORMATION FOR SEQ ID NO:  42:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  73 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-437-667-42

  Query Match             49.3%;  Score 14.8;  DB 2;  Length 73;
  Best Local Similarity   73.1%;  Pred. No. 1.1e+03;
  Matches   19;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          3 AATTGCGGCAAGAAGAATTGTTTCTG 28
              ||| || |||||||  |  ||||| |
Db         55 AATAGCAGCAAGAAATAGGGTTTCGG 30


RESULT 11
US-08-906-955-42/c
; Sequence 42, Application US/08906955
; Patent No. 6013443
;  GENERAL INFORMATION:
;    APPLICANT:  HEILIG, JOSEPH S.
;    APPLICANT:  GOLD, LARRY
;    TITLE OF INVENTION:  SYSTEMATIC EVOLUTION OF LIGANDS BY
;    TITLE OF INVENTION:  EXPONENTIAL ENRICHMENT:  TISSUE
;    TITLE OF INVENTION:  SELEX
;    NUMBER OF SEQUENCES:  240
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Swanson & Bratschun, L.L.C.
;      STREET:  8400 E. Prentice Avenue, Suite 200
;      CITY:  Englewood
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3 1/2 diskette, 1.44 MB
;      COMPUTER:  IBM pc compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/906,955
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/714,131
;      FILING DATE:  10-JUNE-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/434,001
;      FILING DATE:  05-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Barry J. Swanson
;      REGISTRATION NUMBER:  33,215
;      REFERENCE/DOCKET NUMBER:  NEX30-5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 793-3333
;      TELEFAX:  (303) 793-3433
;  INFORMATION FOR SEQ ID NO:  42:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  73 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-906-955-42

  Query Match             49.3%;  Score 14.8;  DB 3;  Length 73;
  Best Local Similarity   73.1%;  Pred. No. 1.1e+03;
  Matches   19;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          3 AATTGCGGCAAGAAGAATTGTTTCTG 28
              ||| || |||||||  |  ||||| |
Db         55 AATAGCAGCAAGAAATAGGGTTTCGG 30


RESULT 12
US-08-945-909-42/c
; Sequence 42, Application US/08945909
; Patent No. 6114120
;  GENERAL INFORMATION:
;    APPLICANT:  JENSEN, KIRK
;    APPLICANT:  CHEN, HANG
;    APPLICANT:  MORRIS, KEVIN
;    APPLICANT:  STEPHENS, ANDREW
;    APPLICANT:  GOLD, LARRY
;    TITLE OF INVENTION:  SYSTEMATIC EVOLUTION OF LIGANDS
;    TITLE OF INVENTION:  ENRICYMENT:  TISSUE SELEX
;    NUMBER OF SEQUENCES:  240
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Swanson & Bratschun, L.L.C.
;      STREET:  8400 E. Prentice Avenue, Suite 200
;      CITY:  Englewood
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3 1/2 diskette, 1.44 MB
;      COMPUTER:  IBM pc compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/945,909
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/06060
;      FILING DATE:  01-MAY-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/434,425
;      FILING DATE:  03-MAY-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/437,667
;      FILING DATE:  03-MAY-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/434,001
;      FILING DATE:  03-MAY-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/433,585
;      FILING DATE:  03-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Barry J. Swanson
```

```
;      REGISTRATION NUMBER:  33,215
;      REFERENCE/DOCKET NUMBER:  NEX30C-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 793-3333
;      TELEFAX:  (303) 793-3433
;  INFORMATION FOR SEQ ID NO:  42:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  73 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-945-909-42

  Query Match             49.3%;  Score 14.8;  DB 3;  Length 73;
  Best Local Similarity   73.1%;  Pred. No. 1.1e+03;
  Matches   19;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          3 AATTGCGGCAAGAAGAATTGTTTCTG 28
              ||| || |||||||  |  ||||| |
Db         55 AATAGCAGCAAGAAATAGGGTTTCGG 30


RESULT 13
US-09-396-002A-42/c
; Sequence 42, Application US/09396002A
; Patent No. 6376474
;  GENERAL INFORMATION:
;       APPLICANT: HEILIG, JOSEPH S.
;                  GOLD, LARRY
;       TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY
;                           EXPONENTIAL ENRICHMENT:  TISSUE SELEX
;       NUMBER OF SEQUENCES: 240
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Swanson & Bratschun, L.L.C.
;            STREET: 1745 Shea Center Drive, Suite 330
;            CITY: Highlands Ranch
;            STATE: Colorado
;            COUNTRY: USA
;            ZIP: 80129
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
;            COMPUTER: IBM pc compatible
;            OPERATING SYSTEM: MS-DOS
;            SOFTWARE: WordPerfect 8.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/396,002A
;            FILING DATE: 14-Sep-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 07/714,131
;            FILING DATE: 10-JUNE-1991
;            APPLICATION NUMBER: 08/434,001
;            FILING DATE: 05-MAY-1995
;            APPLICATION NUMBER: 08/906,955
;            FILING DATE: 05-AUGUST-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Barry J. Swanson
;            REGISTRATION NUMBER: 33,215
;            REFERENCE/DOCKET NUMBER: NEX30-5/D
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (303) 268-0066
;            TELEFAX: (303) 268-0065
;   INFORMATION FOR SEQ ID NO: 42:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 73 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-396-002A-42

  Query Match             49.3%;  Score 14.8;  DB 3;  Length 73;
  Best Local Similarity   73.1%;  Pred. No. 1.1e+03;
  Matches   19;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          3 AATTGCGGCAAGAAGAATTGTTTCTG 28
              ||| || |||||||  |  ||||| |
Db         55 AATAGCAGCAAGAAATAGGGTTTCGG 30


RESULT 14
US-10-077-319-42/c
; Sequence 42, Application US/10077319
; Patent No. 6613526
;  GENERAL INFORMATION:
;       APPLICANT: HEILIG, JOSEPH S.
;                  GOLD, LARRY
;       TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY
;                           EXPONENTIAL ENRICHMENT:  TISSUE SELEX
;       NUMBER OF SEQUENCES: 240
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Swanson & Bratschun, L.L.C.
;            STREET: 1745 Shea Center Drive, Suite 330
;            CITY: Highlands Ranch
;            STATE: Colorado
;            COUNTRY: USA
;            ZIP: 80129
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
;            COMPUTER: IBM pc compatible
;            OPERATING SYSTEM: MS-DOS
;            SOFTWARE: WordPerfect 8.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/077,319
;            FILING DATE: 14-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/396,002
;            FILING DATE: 14-Sep-1999
;            APPLICATION NUMBER: 07/714,131
;            FILING DATE: 10-JUNE-1991
;            APPLICATION NUMBER: 08/434,001
;            FILING DATE: 05-MAY-1995
;            APPLICATION NUMBER: 08/906,955
;            FILING DATE: 05-AUGUST-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Barry J. Swanson
;            REGISTRATION NUMBER: 33,215
;            REFERENCE/DOCKET NUMBER: NEX30-5/D
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (303) 268-0066
;            TELEFAX: (303) 268-0065
;   INFORMATION FOR SEQ ID NO: 42:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 73 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-077-319-42

  Query Match             49.3%;  Score 14.8;  DB 4;  Length 73;
  Best Local Similarity   73.1%;  Pred. No. 1.1e+03;
  Matches   19;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          3 AATTGCGGCAAGAAGAATTGTTTCTG 28
              ||| || |||||||  |  ||||| |
Db         55 AATAGCAGCAAGAAATAGGGTTTCGG 30


RESULT 15
PCT-US96-06060-42/c
; Sequence 42, Application PC/TUS9606060
;  GENERAL INFORMATION:
;    APPLICANT:  JENSEN, KIRK
;    APPLICANT:  CHEN, HANG
```

; APPLICANT: MORRIS, KEVIN
; APPLICANT: STEPHENS, ANDREW
; APPLICANT: GOLD, LARRY
; TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY
; TITLE OF INVENTION: EXPONENTIAL ENRICYMENT: TISSUE
; TITLE OF INVENTION: SELEX
; NUMBER OF SEQUENCES: 240
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
; COMPUTER: IBM pc compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/06060
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/434,425
; FILING DATE: 05-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/437,667
; FILING DATE: 05-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/434,001
; FILING DATE: 05-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/433,585
; FILING DATE: 05-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX30/PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 73 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US96-06060-42

Query Match 49.3%; Score 14.8; DB 5; Length 73;
Best Local Similarity 73.1%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
Qy          3 AATTGCGGCAAGAAGAATTGTTTCTG 28
              ||| || |||||||  |  ||||| |
Db         55 AATAGCAGCAAGAAATAGGGTTTCGG 30
```

Search completed: November 5, 2004, 17:15:09
Job time : 73 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 5, 2004, 15:47:02 ; Search time 344 Seconds
(without alignments)
469.545 Million cell updates/sec

Title: US-09-890-363-1
Perfect score: 30
Sequence: 1 gtaattgcggcaagaagaattgtttctgtc 30

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3611042 seqs, 2692057975 residues

Total number of hits satisfying chosen parameters: 2098264

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	16.2	54.0	60	10	US-09-908-975-8004	Sequence 8004, Ap
	2	15.8	52.7	41	14	US-10-043-573-94	Sequence 94, Appl
c	3	15.8	52.7	47	16	US-10-294-934-510	Sequence 510, App
	4	15.4	51.3	43	15	US-10-032-585-1769	Sequence 1769, Ap
	5	15.4	51.3	65	10	US-09-908-975-30222	Sequence 30222, A
c	6	15.2	50.7	73	15	US-10-403-337-33	Sequence 33, Appl
c	7	15.2	50.7	73	16	US-10-351-890-33	Sequence 33, Appl
c	8	15	50.0	41	16	US-10-035-833A-2017	Sequence 2017, Ap
c	9	15	50.0	41	16	US-10-035-833A-4612	Sequence 4612, Ap
	10	15	50.0	68	13	US-10-027-632-51852	Sequence 51852, A
	11	15	50.0	68	13	US-10-027-632-51860	Sequence 51860, A
	12	15	50.0	68	15	US-10-027-632-51852	Sequence 51852, A
	13	15	50.0	68	15	US-10-027-632-51860	Sequence 51860, A
	14	14.8	49.3	35	15	US-10-125-994A-68	Sequence 68, Appl
c	15	14.8	49.3	43	15	US-10-032-585-1755	Sequence 1755, Ap
	16	14.8	49.3	47	16	US-10-294-934-596	Sequence 596, App
	17	14.8	49.3	65	10	US-09-908-975-1549	Sequence 1549, Ap
	18	14.8	49.3	65	10	US-09-908-975-1579	Sequence 1579, Ap
c	19	14.8	49.3	73	14	US-10-077-319-42	Sequence 42, Appl
c	20	14.6	48.7	21	16	US-10-691-529-49	Sequence 49, Appl
	21	14.6	48.7	50	16	US-10-131-827-3912	Sequence 3912, Ap
	22	14.6	48.7	65	10	US-09-908-975-24143	Sequence 24143, A
	23	14.6	48.7	65	10	US-09-908-975-26971	Sequence 26971, A
c	24	14.6	48.7	65	15	US-10-032-585-2629	Sequence 2629, Ap
	25	14.4	48.0	61	10	US-09-907-111-56	Sequence 56, Appl
c	26	14.2	47.3	21	16	US-10-691-529-199	Sequence 199, App
c	27	14.2	47.3	27	10	US-09-911-904-48	Sequence 48, Appl
c	28	14.2	47.3	39	14	US-10-194-405-2	Sequence 2, Appli
	29	14.2	47.3	60	10	US-09-908-975-7698	Sequence 7698, Ap
	30	14.2	47.3	60	10	US-09-908-975-12139	Sequence 12139, A
	31	14.2	47.3	60	10	US-09-908-975-12670	Sequence 12670, A
	32	14.2	47.3	60	10	US-09-908-975-13972	Sequence 13972, A
	33	14.2	47.3	60	10	US-09-908-975-15633	Sequence 15633, A
	34	14.2	47.3	60	10	US-09-908-975-22515	Sequence 22515, A
	35	14.2	47.3	65	10	US-09-908-975-1807	Sequence 1807, Ap
	36	14.2	47.3	65	10	US-09-908-975-28469	Sequence 28469, A
c	37	14.2	47.3	69	17	US-10-182-040C-4	Sequence 4, Appli
c	38	14.2	47.3	69	17	US-10-182-040C-5	Sequence 5, Appli
c	39	14.2	47.3	69	17	US-10-182-040C-6	Sequence 6, Appli
c	40	14.2	47.3	69	17	US-10-182-040C-7	Sequence 7, Appli
c	41	14	46.7	24	13	US-10-116-288-15	Sequence 15, Appl
	42	14	46.7	25	15	US-10-098-263B-122963	Sequence 122963,
c	43	14	46.7	27	13	US-10-116-288-16	Sequence 16, Appl
c	44	14	46.7	30	13	US-10-116-288-17	Sequence 17, Appl
c	45	14	46.7	33	13	US-10-116-288-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-908-975-8004
; Sequence 8004, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8004
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-8004

Query Match 54.0%; Score 16.2; DB 10; Length 60;
Best Local Similarity 85.7%; Pred. No. 2.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          3 AATTGCGGCAAGAAGAATTGT 23
              || ||| |||||||||| |||
Db         29 AACTGCCGCAAGAAGAAGTGT 49
```

```
RESULT 2
US-10-043-573-94
; Sequence 94, Application US/10043573
; Publication No. US20030032025A1
;   GENERAL INFORMATION:
;        APPLICANT: Lemieux, Bertrand
;                   Landry, Benoit S.
;                   Sapolsky, Ronald J.
;        TITLE OF INVENTION: Brassica Polymorphisms
;        NUMBER OF SEQUENCES: 173
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/043,573
;             FILING DATE: 09-Jan-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/813,507
;             FILING DATE: 07-MAR-1997
;             APPLICATION NUMBER: US 60/032,069
;             FILING DATE: 02-DEC-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Liebeschuetz, Joe
;             REGISTRATION NUMBER: 37,505
;             REFERENCE/DOCKET NUMBER: 018547-030100US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415 576-0200
;             TELEFAX: 415 576-0200
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 94:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 41 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 94:
US-10-043-573-94

  Query Match             52.7%;  Score 15.8;  DB 14;  Length 41;
  Best Local Similarity   74.1%;  Pred. No. 4e+03;
  Matches   20;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          4 ATTGCGGCAAGAAGAATTGTTTCTGTC 30
              |||| | |  || | |||||||||| ||
Db         12 ATTGGGTCTTGATGGATTGTTTCTATC 38


RESULT 3
US-10-294-934-510/c
; Sequence 510, Application US/10294934
; Publication No. US20040038231A1
; GENERAL INFORMATION:
;  APPLICANT: Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Cohen, Annick
;  TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
;  FILE REFERENCE: 62.US4.DIV
;  CURRENT APPLICATION NUMBER: US/10/294,934
;  CURRENT FILING DATE:  2000-09-27
;  PRIOR APPLICATION NUMBER: US 09/671,317
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US 09/536,178
;  PRIOR FILING DATE: 2000-03-23
;  PRIOR APPLICATION NUMBER: PCT/IB00/00403
;  PRIOR FILING DATE: 2000-03-24
;  PRIOR APPLICATION NUMBER: US 60/126,269
;  PRIOR FILING DATE: 1999-03-25
;  PRIOR APPLICATION NUMBER: US 60/131,961
;  PRIOR FILING DATE: 1999-04-30
;  NUMBER OF SEQ ID NOS: 977
;  SOFTWARE: Patent.pm
; SEQ ID NO 510
;   LENGTH: 47
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 24
;   OTHER INFORMATION: 12-456-269 : polymorphic base A or G
US-10-294-934-510

  Query Match             52.7%;  Score 15.8;  DB 16;  Length 47;
  Best Local Similarity   74.1%;  Pred. No. 4.1e+03;
  Matches   20;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          3 AATTGCGGCAAGAAGAATTGTTTCTGT 29
              |||| | || |||||||||  | || |
Db         30 AATTCCYGCTAGAAGAATTCCTGCTCT 4


RESULT 4
US-10-032-585-1769
; Sequence 1769, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
;  APPLICANT: Terry, Roemer D.
;  APPLICANT:  Bo, Jiang
;  APPLICANT:  Charles, Boone
;  APPLICANT:  Howard, Bussey
;  TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
;  FILE REFERENCE: 10182-005-999
;  CURRENT APPLICATION NUMBER: US/10/032,585
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 8000
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1769
;   LENGTH: 43
;   TYPE: DNA
;   ORGANISM: Candida albicans
US-10-032-585-1769

  Query Match             51.3%;  Score 15.4;  DB 15;  Length 43;
  Best Local Similarity   76.0%;  Pred. No. 6e+03;
  Matches   19;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          5 TTGCGGCAAGAAGAATTGTTTCTGT 29
              || || |||||| |||||  ||| |
Db          1 TTACGACAAGAACAATTGAATCTAT 25


RESULT 5
US-09-908-975-30222
; Sequence 30222, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
;  APPLICANT: SHOSHAN, Avi
;  APPLICANT:  WASSERMAN, Alon
;  APPLICANT:  MINTZ, Eli
;  APPLICANT:  MINTZ, Liat
;  APPLICANT:  FAIGLER, Simchon
;  TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
;  TITLE OF INVENTION:  THAT POPULATE A TRANSCRIPTOME
;  FILE REFERENCE: 36688-0005
;  CURRENT APPLICATION NUMBER: US/09/908,975
```

; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30222
; LENGTH: 65
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-908-975-30222

Query Match 51.3%; Score 15.4; DB 10; Length 65;
Best Local Similarity 76.0%; Pred. No. 6.6e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 TAATTGCGGCAAGAAGAATTGTTTC 26
||| |||| | || ||| | |||||
Db 16 TAACTGCGACGAGGAGATTCGTTTC 40

RESULT 6
US-10-403-337-33/c
; Sequence 33, Application US/10403337
; Publication No. US20030215948A1
; GENERAL INFORMATION:
; APPLICANT: Kaleko, Michael
; APPLICANT: Nemerow, Glen R.
; APPLICANT: Smith, Theodore
; APPLICANT: Stevenson, Susan C.
; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting
; FILE REFERENCE: 22908-1236B
; CURRENT APPLICATION NUMBER: US/10/403,337
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: 10/351,890
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/350,388
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/391,967
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; LENGTH: 73
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: amplification primer
US-10-403-337-33

Query Match 50.7%; Score 15.2; DB 15; Length 73;
Best Local Similarity 71.4%; Pred. No. 8.4e+03;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 TAATTGCGGCAAGAAGAATTGTTTCTGT 29
||| || | | |||||| |||| |||
Db 59 TAACTGAAGAATAAAGAATCGTTTGTGT 32

RESULT 7
US-10-351-890-33/c
; Sequence 33, Application US/10351890
; Publication No. US20040002060A1
; GENERAL INFORMATION:
; APPLICANT: Stevenson, Susan C.
; APPLICANT: Kaleko, Michael
; APPLICANT: Smith, Theodore
; APPLICANT: Nemerow, Glen R.
; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting
; FILE REFERENCE: 22908-1236
; CURRENT APPLICATION NUMBER: US/10/351,890
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/350,388
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/391,967
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; LENGTH: 73
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: amplification primer
US-10-351-890-33

Query Match 50.7%; Score 15.2; DB 16; Length 73;
Best Local Similarity 71.4%; Pred. No. 8.4e+03;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 TAATTGCGGCAAGAAGAATTGTTTCTGT 29
||| || | | |||||| |||| |||
Db 59 TAACTGAAGAATAAAGAATCGTTTGTGT 32

RESULT 8
US-10-035-833A-2017/c
; Sequence 2017, Application US/10035833A
; Publication No. US20040072156A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yuho
; APPLICANT: Sekine, Akihiro
; APPLICANT: Iida, Aritoshi
; APPLICANT: Saito, Osamu
; TITLE OF INVENTION: Detection of Genetic Polymorphisms
; FILE REFERENCE: FORS-06904
; CURRENT APPLICATION NUMBER: US/10/035,833A
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 7669
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2017
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-035-833A-2017

Query Match 50.0%; Score 15; DB 16; Length 41;
Best Local Similarity 72.0%; Pred. No. 9e+03;
Matches 18; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 2 TAATTGCGGCAAGAAGAATTGTTTC 26
|| || | |||| | ||:|| ||||
Db 38 TATTTACAGCAATATGAWTTTTTTC 14

RESULT 9
US-10-035-833A-4612/c
; Sequence 4612, Application US/10035833A
; Publication No. US20040072156A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yuho
; APPLICANT: Sekine, Akihiro
; APPLICANT: Iida, Aritoshi
; APPLICANT: Saito, Osamu
; TITLE OF INVENTION: Detection of Genetic Polymorphisms
; FILE REFERENCE: FORS-06904
; CURRENT APPLICATION NUMBER: US/10/035,833A
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 7669
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4612
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-035-833A-4612

```
  Query Match             50.0%;  Score 15;  DB 16;  Length 41;
  Best Local Similarity   72.0%;  Pred. No. 9e+03;
  Matches   18;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 TAATTGCGGCAAGAAGAATTGTTTC 26
              || || | |||| | ||:|| ||||
Db         38 TATTTACAGCAATATGAWTTTTTTC 14


RESULT 10
US-10-027-632-51852
; Sequence 51852, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 51852
;   LENGTH: 68
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-51852

  Query Match             50.0%;  Score 15;  DB 13;  Length 68;
  Best Local Similarity   72.0%;  Pred. No. 1e+04;
  Matches   18;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 TAATTGCGGCAAGAAGAATTGTTTC 26
              ||| || ||||| |||||  : |||
Db         10 TAAATGAGGCAATAAGAAACSATTC 34


RESULT 11
US-10-027-632-51860
; Sequence 51860, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 51860
;   LENGTH: 68
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-51860

  Query Match             50.0%;  Score 15;  DB 13;  Length 68;
  Best Local Similarity   72.0%;  Pred. No. 1e+04;
  Matches   18;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 TAATTGCGGCAAGAAGAATTGTTTC 26
              ||| || ||||| |||||  : |||
Db         10 TAAATGAGGCAATAAGAAACSATTC 34


RESULT 12
US-10-027-632-51852
; Sequence 51852, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 51852
;   LENGTH: 68
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-51852

  Query Match             50.0%;  Score 15;  DB 15;  Length 68;
  Best Local Similarity   72.0%;  Pred. No. 1e+04;
  Matches   18;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 TAATTGCGGCAAGAAGAATTGTTTC 26
              ||| || ||||| |||||  : |||
Db         10 TAAATGAGGCAATAAGAAACSATTC 34


RESULT 13
US-10-027-632-51860
; Sequence 51860, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
```

; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 51860
; LENGTH: 68
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-51860

Query Match 50.0%; Score 15; DB 15; Length 68;
Best Local Similarity 72.0%; Pred. No. 1e+04;
Matches 18; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 2 TAATTGCGGCAAGAAGAATTGTTTC 26
||| || ||||| ||||| : |||
Db 10 TAAATGAGGCAATAAGAAACSATTC 34

RESULT 14
US-10-125-994A-68
; Sequence 68, Application US/10125994A
; Publication No. US20030203427A1
; GENERAL INFORMATION:
; APPLICANT: Koike, Chihiro
; TITLE OF INVENTION: ALPHA 1,3-GALACTOSYLTRANSFERASE GENE AND PROMOTER
; FILE REFERENCE: 206779
; CURRENT APPLICATION NUMBER: US/10/125,994A
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: PCT/US00/29139
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/227,951
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/161,092
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 68
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for identifying murine exons 2 and 3
US-10-125-994A-68

Query Match 49.3%; Score 14.8; DB 15; Length 35;
Best Local Similarity 73.1%; Pred. No. 1.1e+04;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 5 TTGCGGCAAGAAGAATTGTTTCTGTC 30
||| || |||| ||||||||| |
Db 6 TTGAGGATCCAAGACTTGTTTCTGAC 31

RESULT 15
US-10-032-585-1755/c
; Sequence 1755, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1755
; LENGTH: 43
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-032-585-1755

Query Match 49.3%; Score 14.8; DB 15; Length 43;
Best Local Similarity 88.9%; Pred. No. 1.1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 12 AAGAAGAATTGTTTCTGT 29
||||||| |||||| |||
Db 42 AAGAAGACTTGTTTTTGT 25

Search completed: November 5, 2004, 17:21:01
Job time : 347 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 5, 2004, 15:28:19 ; Search time 2315 Seconds
(without alignments)
472.221 Million cell updates/sec

Title: US-09-890-363-1
Perfect score: 30
Sequence: 1 gtaattgcggcaagaagaattgtttctgtc 30

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 389094

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	17.4	58.0	37	8	AZ333195	AZ333195 1M0062G09
	2	15.6	52.0	70	7	T87927	T87927 ye08c07.r1
	3	15.4	51.3	62	1	AL024389	AL024389 r8421a45
c	4	15.4	51.3	67	1	AA591826	AA591826 vi49e12.r
	5	15.4	51.3	70	6	CD881894	CD881894 F1.104K17
c	6	15.4	51.3	70	8	BH865903	BH865903 SALK_1000
c	7	15.4	51.3	75	1	AU014056	AU014056 AU014056
c	8	15.2	50.7	39	8	BH909815	BH909815 SALK_0561
	9	15.2	50.7	49	9	AJ599937	AJ599937 Arabidops
c	10	15.2	50.7	74	1	AA704411	AA704411 zj21h01.s
	11	15.2	50.7	74	7	CF853347	CF853347 psMC008xH
	12	15	50.0	41	8	BH856306	BH856306 SALK_0799
	13	15	50.0	58	1	AA554039	AA554039 nk95g03.s
	14	15	50.0	75	4	BM341762	BM341762 fw52e08.y
	15	14.8	49.3	39	2	BE535115	BE535115 601231231
	16	14.8	49.3	44	8	AZ622559	AZ622559 1M0459P24
	17	14.8	49.3	59	8	BZ769592	BZ769592 SALK_1424
	18	14.8	49.3	60	1	AA388795	AA388795 vb25c07.r
c	19	14.8	49.3	61	1	AI829969	AI829969 wj85b06.x
c	20	14.8	49.3	63	7	N23930	N23930 yx85a12.s1
	21	14.6	48.7	52	2	BF633547	BF633547 NF057G03D
c	22	14.6	48.7	54	8	BH812420	BH812420 SALK_0617
	23	14.6	48.7	62	9	CG667820	CG667820 OST462327
c	24	14.6	48.7	64	4	BI097338	BI097338 SWOv3MCAM
c	25	14.6	48.7	67	9	CC795622	CC795622 SALK_0875
	26	14.6	48.7	69	6	CD028982	CD028982 mgns007xF
	27	14.6	48.7	72	4	BJ057828	BJ057828 BJ057828
c	28	14.6	48.7	73	5	BX697533	BX697533 BX697533
c	29	14.6	48.7	73	6	CB832531	CB832531 SWWbmfCAV
	30	14.6	48.7	73	9	CG495277	CG495277 OST34591
c	31	14.6	48.7	74	7	CN862695	CN862695 000903AAL
c	32	14.6	48.7	75	2	AW247813	AW247813 2820447.3
	33	14.4	48.0	42	1	AU268709	AU268709 AU268709
	34	14.4	48.0	45	6	CA967668	CA967668 CcLL03a10
c	35	14.4	48.0	68	1	AV852289	AV852289 AV852289
	36	14.4	48.0	68	8	AZ921506	AZ921506 1006030C0
c	37	14.4	48.0	73	5	BU870927	BU870927 Q021E02 P
	38	14.4	48.0	74	8	AZ576247	AZ576247 AST-TD14S
	39	14.4	48.0	75	6	CD744649	CD744649 IRB17_A12
	40	14.2	47.3	37	4	BJ066419	BJ066419 BJ066419
	41	14.2	47.3	50	8	BZ664415	BZ664415 SALK_0710
	42	14.2	47.3	50	8	BZ664418	BZ664418 SALK_0711
c	43	14.2	47.3	52	8	AZ694935	AZ694935 TE-389-3
	44	14.2	47.3	54	2	BF450060	BF450060 maa46c07.
c	45	14.2	47.3	54	8	BZ761965	BZ761965 SALK_0837

ALIGNMENTS

RESULT 1
AZ333195/c
LOCUS AZ333195 37 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0062G09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0062G09 F, genomic survey sequence.
ACCESSION AZ333195
VERSION AZ333195.1 GI:10397573
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 37)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0062 row: G column: 09
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 37.
FEATURES Location/Qualifiers
source 1. .37
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0062G09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 58.0%; Score 17.4; DB 8; Length 37;
Best Local Similarity 77.8%; Pred. No. 5.7e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 TAATTGCGGCAAGAAGAATTGTTTCTG 28
||||||||||||||||||||||||||||
Db 32 TAATTGAGGGAAGAAGATGTGGTTTTG 6

RESULT 2
T87927
LOCUS T87927 70 bp mRNA linear EST 17-MAR-1995
DEFINITION ye08c07.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:117132 5' similar to gb:M68519_rna1 PULMONARY SURFACTANT-ASSOCIATED PROTEIN A PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION T87927
VERSION T87927.1 GI:716279
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 70)
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
MEDLINE 97044478
PUBMED 8889549
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 570
High quality sequence starts: 1 High quality sequence stops: 1
Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality
Insert Length: 570 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .70
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:485421"
/db_xref="taxon:9606"
/clone="IMAGE:117132"
/sex="male"
/dev_stage="72 years"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene lung (#937210)"
/note="Organ: lung; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. normal lung. Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
ORIGIN

Query Match 52.0%; Score 15.6; DB 7; Length 70;
Best Local Similarity 70.0%; Pred. No. 3.9e+04;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GTAATTGCGGCAAGAAGAATTGTTTCTGTC 30
|||| | ||||| | ||||| |||||
Db 31 GAAATAGGAATAAGAATACTTGTTGCTGTC 60

RESULT 3
AL024389
LOCUS AL024389 62 bp mRNA linear EST 29-DEC-1999
DEFINITION r8421a45 Beddington mouse dissected endoderm Mus musculus cDNA clone 528-7J11 5', mRNA sequence.
ACCESSION AL024389
VERSION AL024389.1 GI:6646057
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 62)
AUTHORS Harrison,S.M., Dunwoodie,S.L., Arkell,R.M., Lehrach,H. and Beddington,R.S.
TITLE Isolation of novel tissue-specific genes from cDNA libraries representing the individual tissue constituents of the gastrulating mouse embryo
JOURNAL Development 121 (8), 2479-2489 (1995)
MEDLINE 95401865
PUBMED 7671812
COMMENT Contact: Wiles,M., Lehrach,H. and Avner,P.
EEC Mouse Transcript Mapping Consortium
Genoscope - CNS
2, rue Gaston Cremieux, 91000 Evry, France
Email: pavner@pasteur.fr
clone available from Ressourcenzentrum, Heubnerweg 6, D-14059 Berlin, Germany. Web site http://www.rzpd.de
Seq primer: CCGGTCCGGAATTCCCGGGT;
High quality sequence only submitted.
Vector: pSport1; site_1: NotI; site_2: SalI;
Cloned unidirectionally.
Dissected endoderm 7.5 days.
Average insert size: 1.2 kb (range: 0.2 - 2.kb).
FEATURES Location/Qualifiers
source 1. .62
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6 x DBA"
/db_xref="taxon:10090"
/clone="528-7J11"
/tissue_type="dissected endoderm"
/dev_stage="7.5 dpc"
/clone_lib="Beddington mouse dissected endoderm"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI; Cloned unidirectionally.~ High quality sequence only submitted.~ Average insert size: 1.2 kb (range: 0.2 - 2.kb)"
ORIGIN

Query Match 51.3%; Score 15.4; DB 1; Length 62;
Best Local Similarity 76.0%; Pred. No. 4.7e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GTAATTGCGGCAAGAAGAATTGTTT 25

```
                  | | ||| || ||||||||||  ||
Db         23 GGAGTTGTGGGAAGAAGAATTTATT 47


RESULT 4
AA591826/c
LOCUS       AA591826                 67 bp    mRNA    linear   EST 16-SEP-1997
DEFINITION  vi49e12.r1 Beddington mouse embryonic region Mus musculus cDNA
            clone IMAGE:907150 5' similar to gb:X61399 Mouse F52 mRNA for a
            novel protein (MOUSE);, mRNA sequence.
ACCESSION   AA591826
VERSION     AA591826.1  GI:2405489
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 67)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:527814
            Trace considered overall poor quality
            Putative full length read
            vector to vector length is 111
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .67
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6 x DBA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:907150"
                     /sex="pooled"
                     /tissue_type="embryo"
                     /dev_stage="7.5dpc"
                     /lab_host="DH12S"
                     /clone_lib="Beddington mouse embryonic region"
                     /note="Organ: whole embryo; Vector: pCMV-SPORT; Site_1:
                     SalI; Site_2: NotI; Cloned unidirectionally.  Primer:
                     Oligo dT. Gastrulating embryos were collected at 7.5dpc
                     from C57BL6 x DBA matings, excluding embryos that had
                     developed head folds and all extraembryonic tissues.
                     Average insert size: 1.3 kb (range: 0.5 - 3.0 kb).
                     Referenced in Development 121, 2479-2489 (1995)"
ORIGIN

  Query Match             51.3%;  Score 15.4;  DB 1;  Length 67;
  Best Local Similarity   76.0%;  Pred. No. 4.7e+04;
  Matches   19;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 GTAATTGCGGCAAGAAGAATTGTTT 25
              |||| | |||   ||||||| ||||
Db         31 GTAAATCCGGGTGGAAGAATGGTTT 7


RESULT 5
CD881894
LOCUS       CD881894                 70 bp    mRNA    linear   EST 14-JUL-2003
DEFINITION  F1.104K17F010329 F1 Triticum aestivum cDNA clone F1104K17, mRNA
            sequence.
ACCESSION   CD881894
VERSION     CD881894.1  GI:32642165
KEYWORDS    EST.
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 70)
  AUTHORS   Genoplante.
  TITLE     Genoplante, a major partnership french program in plant genomics
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Genoplante
            Genoplante
            93, rue Henri Rochefort 91025 EVRY CEDEX France
            Tel: 33 1 69 47 54 00
            Fax: 33 1 69 47 54 10
            This sequence has been generated in the framework of the french
            plant genomics programme 'Genoplante' (http://www.genoplante.com
            and http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .70
                     /organism="Triticum aestivum"
                     /mol_type="mRNA"
                     /cultivar="recital"
                     /db_xref="taxon:4565"
                     /clone="F1104K17"
                     /tissue_type="leaf one"
                     /clone_lib="F1"
ORIGIN

  Query Match             51.3%;  Score 15.4;  DB 6;  Length 70;
  Best Local Similarity   94.1%;  Pred. No. 4.8e+04;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         14 GAAGAATTGTTTCTGTC 30
              || |||||||||||||||
Db         14 GAGGAATTGTTTCTGTC 30


RESULT 6
BH865903/c
LOCUS       BH865903                 70 bp    DNA     linear   GSS 05-AUG-2002
DEFINITION  SALK_100053 Arabidopsis thaliana TDNA insertion lines Arabidopsis
            thaliana genomic clone SALK_100053, genomic survey sequence.
ACCESSION   BH865903
VERSION     BH865903.1  GI:22101801
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 70)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA. This sequence lies within an annotated exon of At4g32010.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
```

```
     source          1. .70
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /ecotype="Col-0"
                     /db_xref="taxon:3702"
                     /clone="SALK_100053"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
ORIGIN

  Query Match             51.3%;  Score 15.4;  DB 8;  Length 70;
  Best Local Similarity   76.0%;  Pred. No. 4.8e+04;
  Matches   19;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          3 AATTGCGGCAAGAAGAATTGTTTCT 27
              || ||   |||||||||| ||| ||
Db         35 AAATGAAACAAGAAGAATCGTTGCT 11


RESULT 7
AU014056/c
LOCUS       AU014056                  75 bp    mRNA    linear   EST 03-AUG-1998
DEFINITION  AU014056 Schizosaccharomyces pombe late log phase cDNA
            Schizosaccharomyces pombe cDNA clone spc09062, mRNA sequence.
ACCESSION   AU014056
VERSION     AU014056.1  GI:3368847
KEYWORDS    EST.
SOURCE      Schizosaccharomyces pombe (fission yeast)
  ORGANISM  Schizosaccharomyces pombe
            Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
            Schizosaccharomycetales; Schizosaccharomycetaceae;
            Schizosaccharomyces.
REFERENCE   1  (bases 1 to 75)
  AUTHORS   Morimyo,M. and Mita,K.
  TITLE     Identification of expressed sequence tags of Schizosaccharomyces
            pombe
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Mitsuoki Morimyo
            Genome Research Group
            National Institute of Radiological Sciences
            9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
            Email: morimyo@nirs.go.jp.
FEATURES             Location/Qualifiers
     source          1. .75
                     /organism="Schizosaccharomyces pombe"
                     /mol_type="mRNA"
                     /strain="972"
                     /db_xref="taxon:4896"
                     /clone="spc09062"
                     /sex="h minus"
                     /clone_lib="Schizosaccharomyces pombe late log phase cDNA"
                     /note="Vector: M13mp19; The cDNA library of
                     Schizosaccharomyces pombe was prepared by cloning cDNA
                     into the SmaI site of M13mp19 DNA and the direction of DNA
                     sequences was not always from 5' to 3'. The cDNA data of
                     Schizosaccharomyces pombe are available for searching on
                     the World Wide Web.  (URL, http://www.nirs.go.jp)"
ORIGIN

  Query Match             51.3%;  Score 15.4;  DB 1;  Length 75;
  Best Local Similarity   76.0%;  Pred. No. 4.8e+04;
  Matches   19;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          5 TTGCGGCAAGAAGAATTGTTTCTGT 29
              || ||| || || ||||||||  ||
Db         70 TTACGGGAAAAATAATTGTTTAGGT 46


RESULT 8
BH909815/c
LOCUS       BH909815                  39 bp    DNA     linear   GSS 04-SEP-2002
DEFINITION  SALK_056115.47.35.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_056115.47.35.x, genomic
            survey sequence.
ACCESSION   BH909815
VERSION     BH909815.1  GI:22722748
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /ecotype="Col-0"
                     /db_xref="taxon:3702"
                     /clone="SALK_056115.47.35.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
ORIGIN

  Query Match             50.7%;  Score 15.2;  DB 8;  Length 39;
  Best Local Similarity   71.4%;  Pred. No. 5.4e+04;
  Matches   20;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          2 TAATTGCGGCAAGAAGAATTGTTTCTGT 29
              ||||| |   ||||| |||   ||||||
Db         37 TAATTACATAAAGAATAATATGTTCTGT 10


RESULT 9
AJ599937
LOCUS       AJ599937                  49 bp    DNA     linear   GSS 15-JAN-2004
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
            496H09, genomic survey sequence.
ACCESSION   AJ599937
VERSION     AJ599937.1  GI:37949565
KEYWORDS    GSS; left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
```

```
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 49)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="496H09"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .49
                     /note="T-DNA flanking sequence
                     left border"
ORIGIN

  Query Match             50.7%;  Score 15.2;  DB 9;  Length 49;
  Best Local Similarity   71.4%;  Pred. No. 5.6e+04;
  Matches   20;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          2 TAATTGCGGCAAGAAGAATTGTTTCTGT 29
              || ||| || | | ||||| ||| |||
Db         15 TAGTTGTGGAATGTAGAATCCTTTTTGT 42


RESULT 10
AA704411/c
LOCUS       AA704411                 74 bp    mRNA    linear   EST 24-DEC-1997
DEFINITION  zj21h01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA
            clone IMAGE:450961 3', mRNA sequence.
ACCESSION   AA704411
VERSION     AA704411.1  GI:2714329
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 74)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
            Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
            Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-NCI human EST Project
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 52.
FEATURES             Location/Qualifiers
     source          1. .74
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:1387317"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:450961"
                     /sex="male"
                     /dev_stage="20 week-post conception fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
                     /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                     with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                     This is a subtracted version of the original Soares fetal
                     liver spleen 1NFLS library.  1st strand cDNA was primed
                     with a Pac I - oligo(dT) primer [5'
                     AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Pac I and cloned into the Pac I
                     and Eco RI sites of the modified pT7T3 vector.  Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
ORIGIN

  Query Match             50.7%;  Score 15.2;  DB 1;  Length 74;
  Best Local Similarity   71.4%;  Pred. No. 5.9e+04;
  Matches   20;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          3 AATTGCGGCAAGAAGAATTGTTTCTGTC 30
              | ||  ||||| || | || ||| ||||
Db         34 ATTTATGGCAATAAAATTTTTTTTTGTC 7


RESULT 11
CF853347
LOCUS       CF853347                 74 bp    mRNA    linear   EST 30-OCT-2003
DEFINITION  psMC008xH16f USDA-IFAFS:Expression of Phytophthora sojae genes
            during infection and propagation_sMC Phytophthora sojae cDNA clone
            sMC008H16 5, mRNA sequence.
ACCESSION   CF853347
VERSION     CF853347.1  GI:38069001
KEYWORDS    EST.
SOURCE      Phytophthora sojae
  ORGANISM  Phytophthora sojae
            Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
            Phytophthora.
REFERENCE   1  (bases 1 to 74)
  AUTHORS   Tyler,B.
  TITLE     Tyler,B. Not Published
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Tyler B
            Tyler lab
            VBI
            1880 Pratt Dr., Blacksburg, VA 24061, USA
            Tel: 540-231-7318
            Email: bmtyler@vt.edu
            PCR PRimers
            FORWARD: M13 reverse 17mer at 5' end
            BACKWARD: M13 reverse 17mer at 5' end
            Plate: 008  row: H  column: 16
            Seq primer: M13 reverse 17mer at 5' end
            High quality sequence stop: 74.
FEATURES             Location/Qualifiers
     source          1. .74
                     /organism="Phytophthora sojae"
                     /mol_type="mRNA"
                     /db_xref="taxon:67593"
                     /clone="sMC008H16"
                     /tissue_type="mycelium"
                     /cell_line="P6497"
                     /dev_stage="mycelium"
                     /lab_host="synthetic medium"
                     /clone_lib="USDA-IFAFS:Expression of Phytophthora sojae
                     genes during infection and propagation_sMC"
```

```
                     /note="Vector: pCMV-SPORT6.1; Site_1: Sal1; Site_2: Not1"
ORIGIN

  Query Match             50.7%;  Score 15.2;  DB 7;  Length 74;
  Best Local Similarity   85.0%;  Pred. No. 5.9e+04;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 AATTGCGGCAAGAAGAATTG 22
              || ||| |||||||||| ||
Db         31 AACTGCCGCAAGAAGAAATG 50


RESULT 12
BH856306
LOCUS       BH856306                 41 bp    DNA     linear   GSS 08-JUL-2002
DEFINITION  SALK_079956.50.05.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_079956.50.05.x, genomic
            survey sequence.
ACCESSION   BH856306
VERSION     BH856306.1  GI:21705896
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .41
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /ecotype="Col-0"
                     /db_xref="taxon:3702"
                     /clone="SALK_079956.50.05.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
ORIGIN

  Query Match             50.0%;  Score 15;  DB 8;  Length 41;
  Best Local Similarity   78.3%;  Pred. No. 6.7e+04;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 TAATTGCGGCAAGAAGAATTGTT 24
              |||||  || ||||| |||| ||
Db          3 TAATTTAGGAAAGAATAATTTTT 25


RESULT 13
AA554039
LOCUS       AA554039                 58 bp    mRNA    linear   EST 09-SEP-1997
DEFINITION  nk95g03.s1 NCI_CGAP_Co11 Homo sapiens cDNA clone IMAGE:1028596 3'
            similar to SW:ATP6_HUMAN P00846 ATP SYNTHASE A CHAIN ;, mRNA
            sequence.
ACCESSION   AA554039
VERSION     AA554039.1  GI:2324578
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 58)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Elias Campo,
            M.D., Michael R. Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Stratagene, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 1186   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .58
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1028596"
                     /tissue_type="tumor"
                     /lab_host="SOLR (kanamycin resistant)"
                     /clone_lib="NCI_CGAP_Co11"
                     /note="Organ: colon; Vector: Bluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. Multiple colon tumors. 5' adaptor sequence: 5'
                     GAATTCGGCACGAG 3' 3' adaptor sequence: 5'
                     CTCGAGTTTTTTTTTTTTTTTT 3' Average insert size:  1.1 kb."
ORIGIN

  Query Match             50.0%;  Score 15;  DB 1;  Length 58;
  Best Local Similarity   78.3%;  Pred. No. 7e+04;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 TAATTGCGGCAAGAAGAATTGTT 24
              |||||  || ||||| |||| ||
Db         25 TAGTTGTGGCAATAACAATGGTT 47


RESULT 14
BM341762
LOCUS       BM341762                 75 bp    mRNA    linear   EST 07-JAN-2002
DEFINITION  fw52e08.y1 Zebrafish SJD day 3 embryo Danio rerio cDNA clone
            IMAGE:5568470 5', mRNA sequence.
ACCESSION   BM341762
VERSION     BM341762.1  GI:18078462
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 75)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
            Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
```

```
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library construction by: Joe Barnes and Steve Johnson. DNA
            Sequencing by: Washington University Genome Sequencing Center Clone
            distribution: Research Genetics web address:
            http://www.researchgenetics.com/
            Putative full length read
            The vector to vector length is 76
            Seq primer: T3 ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .75
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /strain="SJD"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:5568470"
                     /tissue_type="embryo, day 3"
                     /lab_host="DH10B"
                     /clone_lib="Zebrafish SJD day 3 embryo"
                     /note="Vector: pAMP1; Site_1: EcoRI; Site_2: NotI; First
                     strand cDNA synthesis was primed using oligo-dT on
                     magnetic beads with an additional primer
                     5'-gcggccgctaatacgactcacta-taggg-3'. Second strand
                     synthesis was a 3-cycle PCR using the primers
                     5'-ggccgctaatacgactcactatag-3' and
                     5'-aagcagtggtaacaacgcagagtacttt-ttttttttttttvn-3'. cDNA
                     was subsequently amplified in a 7-cycle PCR with the
                     following primers: 5'-ggccgctaatacgactcactatag-3' and
                     5'-aagcagtggt-aacaacgcag. Deoxy-UMP adaptors were added in
                     a third PCR (5 cycles) and the primers
                     5'-caucaucaucauggccgctaatacgactcactataggg-3' and
                     5'-cuacuacuacuaaagcagtggtaacaacgcagagtac-3'. Ends were
                     treated with uracil DNA glycosylase and product with 3'
                     overhangs was annealed to complementary ends of pAMP1.
                     Insert can be excised using EcoRI and NotI. Library
                     constructed by Joe Barnes and Steve Johnson (Washington
                     University)."
ORIGIN

  Query Match             50.0%;  Score 15;  DB 4;  Length 75;
  Best Local Similarity   78.3%;  Pred. No. 7.2e+04;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 AATTGCGGCAAGAAGAATTGTTT 25
              ||||  |  |||||| |||||||
Db         12 AATTTAGAAAAGAAGGATTGTTT 34


RESULT 15
BE535115
LOCUS       BE535115                 39 bp    mRNA    linear   EST 09-AUG-2000
DEFINITION  601231231F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:3595207 5',
            mRNA sequence.
ACCESSION   BE535115
VERSION     BE535115.1  GI:9763760
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey Green M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM8770  row: n  column: 08
            High quality sequence stop: 37.
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:3595207"
                     /sex="female, virgin"
                     /tissue_type="infiltrating ductal carcinoma"
                     /dev_stage="5 months"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Mam6"
                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigator
                     providing samples: Jeffrey Green, M.D., NIH"
ORIGIN

  Query Match             49.3%;  Score 14.8;  DB 2;  Length 39;
  Best Local Similarity   73.1%;  Pred. No. 8.2e+04;
  Matches   19;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          3 AATTGCGGCAAGAAGAATTGTTTCTG 28
              |||   |||||||| ||||| |  ||
Db          5 AATAAAGGCAAGAAAAATTGCTGATG 30


Search completed: November  5, 2004, 17:13:58
Job time : 2324 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 5, 2004, 20:41:18 ; Search time 43 Seconds
(without alignments)
157.312 Million cell updates/sec

Title: US-09-882-434A-1
Perfect score: 551
Sequence: 1 MASTKLFFSVITVMMLIAMA.....FGSSARACNPFGWKSIFIQC 102

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	75.5	13.7	486	4	US-08-169-613A-2	Sequence 2, Appli
2	75.5	13.7	486	4	US-08-622-191-8	Sequence 8, Appli
3	74.5	13.5	486	1	US-07-872-678A-48	Sequence 48, Appl
4	74.5	13.5	908	4	US-08-714-741-44	Sequence 44, Appl
5	71	12.9	1280	4	US-09-672-810-2	Sequence 2, Appli
6	71	12.9	1283	4	US-09-672-810-4	Sequence 4, Appli
7	70	12.7	365	4	US-09-252-991A-30166	Sequence 30166, A
8	69	12.5	491	4	US-09-248-796A-17049	Sequence 17049, A
9	69	12.5	1280	4	US-09-672-810-7	Sequence 7, Appli
10	69	12.5	1280	4	US-09-672-725C-4	Sequence 4, Appli
11	69	12.5	1280	4	US-10-044-671-2	Sequence 2, Appli
12	69	12.5	1281	4	US-09-672-725C-2	Sequence 2, Appli
13	69	12.5	1281	4	US-09-672-725C-23	Sequence 23, Appl
14	69	12.5	1281	4	US-09-672-725C-25	Sequence 25, Appl
15	69	12.5	1281	4	US-09-672-725C-27	Sequence 27, Appl
16	68	12.3	1280	2	US-08-583-276-19	Sequence 19, Appl
17	68	12.3	1280	2	US-08-752-447-2	Sequence 2, Appli
18	68	12.3	1280	3	US-09-316-167-2	Sequence 2, Appli
19	68	12.3	1280	4	US-09-767-594-2	Sequence 2, Appli
20	68	12.3	1280	4	US-09-672-810-5	Sequence 5, Appli
21	68	12.3	1280	4	US-09-397-233-2	Sequence 2, Appli
22	68	12.3	1280	4	US-09-672-725C-7	Sequence 7, Appli
23	68	12.3	1280	6	5206352-4	Patent No. 5206352
24	67.5	12.3	312	4	US-09-252-991A-19374	Sequence 19374, A
25	67.5	12.3	459	4	US-09-328-352-4648	Sequence 4648, Ap
26	67.5	12.3	902	1	US-08-701-846-2	Sequence 2, Appli
27	66	12.0	115	4	US-09-252-991A-28403	Sequence 28403, A
28	65	11.8	730	4	US-09-107-532A-4752	Sequence 4752, Ap
29	64.5	11.7	139	4	US-09-252-991A-19245	Sequence 19245, A
30	64.5	11.7	486	4	US-08-622-191-7	Sequence 7, Appli
31	64	11.6	1576	4	US-09-562-702A-24	Sequence 24, Appl
32	64	11.6	1576	4	US-09-561-818A-24	Sequence 24, Appl
33	64	11.6	1584	4	US-09-562-702A-28	Sequence 28, Appl
34	64	11.6	1609	4	US-09-562-702A-22	Sequence 22, Appl
35	64	11.6	1609	4	US-09-561-818A-22	Sequence 22, Appl
36	64	11.6	1609	4	US-09-538-092-900	Sequence 900, App
37	64	11.6	1617	4	US-09-562-702A-26	Sequence 26, Appl
38	63.5	11.5	1019	1	US-08-296-014A-4	Sequence 4, Appli
39	63.5	11.5	1019	2	US-08-596-405-4	Sequence 4, Appli
40	63.5	11.5	1019	2	US-08-877-620-4	Sequence 4, Appli
41	63.5	11.5	1019	4	US-09-287-368-4	Sequence 4, Appli
42	63.5	11.5	1019	4	US-09-626-795-4	Sequence 4, Appli
43	63.5	11.5	1083	1	US-08-296-014A-2	Sequence 2, Appli
44	63.5	11.5	1083	2	US-08-596-405-2	Sequence 2, Appli
45	63.5	11.5	1083	2	US-08-877-620-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-169-613A-2
; Sequence 2, Application US/08169613A
; Patent No. 6486380
; GENERAL INFORMATION:
; APPLICANT: Epstein, Paul
; TITLE OF INVENTION: Pancreatic B Cell Hexokinase Transgene
; FILE REFERENCE: P0044US0
; CURRENT APPLICATION NUMBER: US/08/169,613A
; CURRENT FILING DATE: 1993-12-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 486
; TYPE: PRT
; ORGANISM: yeast
US-08-169-613A-2

Query Match 13.7%; Score 75.5; DB 4; Length 486;
Best Local Similarity 30.2%; Pred. No. 1.7;
Matches 29; Conservative 9; Mismatches 27; Indels 31; Gaps 6;

```
Qy          8 FSVITVMM---LIAMASEMVNGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYDFSYTG 64
              | : | :    ||   ||::                || | | || :|| || ||    ||
Db        369 FGINTTVQERKLIRRLSELIGA------------RAARLSVCGIAAICQKRGYK---TG 412

Qy         65 QTAALYNQAGCSGVAHTRF-GSSARACNP----FGW 95
                ||        |  : |: |   :| |     :||
Db        413 HIAA-------DGSVYNRYPGFKEKAANALKDIYGW 441
```

RESULT 2
US-08-622-191-8
; Sequence 8, Application US/08622191A
; Patent No. 6632602
; GENERAL INFORMATION:
; APPLICANT: Sheen, Jen
; APPLICANT: Jang, Jyan-Chyun
; TITLE OF INVENTION: PLANT SUGAR SENSORS AND USES THEREOF
; FILE REFERENCE: 00786/307001
; CURRENT APPLICATION NUMBER: US/08/622,191A
; CURRENT FILING DATE: 1996-03-25
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 486
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-08-622-191-8

```
  Query Match             13.7%;  Score 75.5;  DB 4;  Length 486;
  Best Local Similarity   30.2%;  Pred. No. 1.7;
  Matches   29;  Conservative    9;  Mismatches   27;  Indels   31;  Gaps    6;

Qy          8 FSVITVMM---LIAMASEMVNGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYDFSYTG 64
              | : | :    ||   ||::                ||  |  |  ||  :|| ||  ||    ||
Db        369 FGINTTVQERKLIRRLSELIGA-------------RAARLSVCGIAAICQKRGYK---TG 412

Qy         65 QTAALYNQAGCSGVAHTRF-GSSARACNP----FGW 95
                ||          |  : |: |   :| |     :||
Db        413 HIAA-------DGSVYNRYPGFKEKAANALKDIYGW 441


RESULT 3
US-07-872-678A-48
; Sequence 48, Application US/07872678A
; Patent No. 5541060
;  GENERAL INFORMATION:
;    APPLICANT:  Bell, Graeme, et al.
;    TITLE OF INVENTION:  DETECTION OF EARLY-ONSET
;    TITLE OF INVENTION:  NON-INSULIN-DEPENDENT DIABETES MELLITUS
;    NUMBER OF SEQUENCES:  48
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  Post Office Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  USA
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/872,678A
;      FILING DATE:  22-APRIL-1992
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coughlin, Daniel F.
;      REGISTRATION NUMBER:  36,111
;      REFERENCE/DOCKET NUMBER:  ARCD016
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713-787-1400
;      TELEFAX:  713-789-2679
;      TELEX:  79-0924
;  INFORMATION FOR SEQ ID NO:  48:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  486 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-872-678A-48

  Query Match             13.5%;  Score 74.5;  DB 1;  Length 486;
  Best Local Similarity   39.3%;  Pred. No. 2.2;
  Matches   24;  Conservative    4;  Mismatches   18;  Indels   15;  Gaps    4;

Qy         40 RAERYSKCGCSAIHQKGGYDFSYTGQTAALYNQAGCSGVAHTRF-GSSARACNP----FG 94
              || | | || :|| || ||    ||  ||        |   ||: |   :| |     :|
Db        391 RAARLSVCGIAAICQKRGYK---TGHIAA-------DGSVSTRYPGFKEKAANALKDIYG 440

Qy         95 W 95
              |
Db        441 W 441


RESULT 4
US-08-714-741-44
; Sequence 44, Application US/08714741
; Patent No. 6500613
;  GENERAL INFORMATION:
;    APPLICANT:  Briles, David E.
;    APPLICANT:  McDaniel, Larry S.
;    APPLICANT:  Swiatlo, Edwin
;    APPLICANT:  Yother, Janet
;    APPLICANT:  Crain, Marilyn J.
;    APPLICANT:  Hollingshead, Susan
;    APPLICANT:  Tart, Rebecca
;    APPLICANT:  Brooks-Walter, Alexis
;    TITLE OF INVENTION:  PNEUMOCOCCAL GENES, PORTIONS THEREOF,
;    TITLE OF INVENTION:  EXPRESSION PRODUCTS THEREFROM, AND USES OF SUCH GENES,
;    TITLE OF INVENTION:  PORTIONS AND PRODUCTS
;    NUMBER OF SEQUENCES:  47
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford, P.C.
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/714,741
;      FILING DATE:  16-SEP-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer Esq., William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454312-2460
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;  INFORMATION FOR SEQ ID NO:  44:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  908 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-714-741-44

  Query Match             13.5%;  Score 74.5;  DB 4;  Length 908;
  Best Local Similarity   34.2%;  Pred. No. 4.8;
  Matches   25;  Conservative    6;  Mismatches   39;  Indels    3;  Gaps    2;

Qy         18 AMASEMVNGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYDFSYTGQTAALYNQAGCSG 77
              | |     |:|    :  ||   |   :  || |     |     || |||    |||:|
Db        240 AAACTATTGAAAAATTAAGC--AAGCAAAAGCGAAAGTTGAGAGCTGCTAAA-AAAGCTG 296

Qy         78 VAHTRFGSSARAC 90
                 | |   ::| ||
Db        297 AATTAGAAAAAAC 309


RESULT 5
US-09-672-810-2
; Sequence 2, Application US/09672810
; Patent No. 6617450
; GENERAL INFORMATION:
;  APPLICANT:  STOCKER, PENNY J.
;  APPLICANT:  STEIMEL-CRESPI, DOROTHY T.
;  APPLICANT:  CRESPI, CHARLES L.
;  TITLE OF INVENTION:  P-GLYCOPROTEINS AND USES THEREOF
;  FILE REFERENCE:  G0307/7018
;  CURRENT APPLICATION NUMBER: US/09/672,810
;  CURRENT FILING DATE:  2000-09-28
;  PRIOR APPLICATION NUMBER:  US 60/156,921
;  PRIOR FILING DATE:  1999-09-28
;  PRIOR APPLICATION NUMBER:  US 60/158,818
;  PRIOR FILING DATE:  1999-10-12
```

; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Macaca fascicularis
US-09-672-810-2

Query Match 12.9%; Score 71; DB 4; Length 1280;
Best Local Similarity 25.5%; Pred. No. 19;
Matches 25; Conservative 12; Mismatches 33; Indels 28; Gaps 3;

```
Qy          6 LFFSVITVMMLIAMASEMV------NGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYD 59
              :||||:     :  ||  :      |:|| ::       : ||| |    : ||  :
Db        334 VFFSVLIGAFSVGQASPSIEAFANARGAAFEIFKIIDNKPSIDSYSKSGHKPDNIKGNLE 393

Qy         60 -----FSY----------------TGQTAALYNQAGC 75
                   |||                :||| ||   :||
Db        394 FRNVHFSYPSRKEVKILKGLNLKVQSGQTVALVGNSGC 431
```

RESULT 6
US-09-672-810-4
; Sequence 4, Application US/09672810
; Patent No. 6617450
; GENERAL INFORMATION:
; APPLICANT: STOCKER, PENNY J.
; APPLICANT: STEIMEL-CRESPI, DOROTHY T.
; APPLICANT: CRESPI, CHARLES L.
; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
; FILE REFERENCE: G0307/7018
; CURRENT APPLICATION NUMBER: US/09/672,810
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/156,921
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/158,818
; PRIOR FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 1283
; TYPE: PRT
; ORGANISM: Macaca fascicularis
US-09-672-810-4

Query Match 12.9%; Score 71; DB 4; Length 1283;
Best Local Similarity 25.5%; Pred. No. 19;
Matches 25; Conservative 12; Mismatches 33; Indels 28; Gaps 3;

```
Qy          6 LFFSVITVMMLIAMASEMV------NGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYD 59
              :||||:     :  ||  :      |:|| ::       : ||| |    : ||  :
Db        337 VFFSVLIGAFSVGQASPSIEAFANARGAAFEIFKIIDNKPSIDSYSKSGHKPDNIKGNLE 396

Qy         60 -----FSY----------------TGQTAALYNQAGC 75
                   |||                :||| ||   :||
Db        397 FRNVHFSYPSRKEVKILKGLNLKVQSGQTVALVGNSGC 434
```

RESULT 7
US-09-252-991A-30166
; Sequence 30166, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30166
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30166

Query Match 12.7%; Score 70; DB 4; Length 365;
Best Local Similarity 27.8%; Pred. No. 5.2;
Matches 22; Conservative 7; Mismatches 46; Indels 4; Gaps 2;

```
Qy         17 IAMASEMVNGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYDFSYTGQTAALYNQAGCS 76
              :| | :  : : |    ||||     | : ||          ||   | ||     |    |
Db        166 LACAVDATSAAVFAGKPGPGCGRSCVRPAICGWEDTGTSGG---SSTGGAETLAGSRACV 222

Qy         77 GVA-HTRFGSSARACNPFG 94
                 |       : || :| |
Db        223 DAATRAETAGACRATDPDG 241
```

RESULT 8
US-09-248-796A-17049
; Sequence 17049, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 17049
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-17049

Query Match 12.5%; Score 69; DB 4; Length 491;
Best Local Similarity 39.4%; Pred. No. 9.8;
Matches 13; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

```
Qy         40 RAERYSKCGCSAIHQKGGYDFSYTGQTAALYNQ 72
              |: |:| || :|| || ||  ::     ::||:
Db        398 RSARFSVCGIAAICQKRGYKTAHCAADGSVYNK 430
```

RESULT 9
US-09-672-810-7
; Sequence 7, Application US/09672810
; Patent No. 6617450
; GENERAL INFORMATION:
; APPLICANT: STOCKER, PENNY J.
; APPLICANT: STEIMEL-CRESPI, DOROTHY T.
; APPLICANT: CRESPI, CHARLES L.
; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
; FILE REFERENCE: G0307/7018
; CURRENT APPLICATION NUMBER: US/09/672,810
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/156,921
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/158,818
; PRIOR FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Canis familiaris

US-09-672-810-7

Query Match 12.5%; Score 69; DB 4; Length 1280;
Best Local Similarity 25.5%; Pred. No. 32;
Matches 25; Conservative 12; Mismatches 33; Indels 28; Gaps 3;

```
Qy          6 LFFSVITVMMLIAMASEMV------NGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYD 59
              :||||:     |  ||  :       |:|: ::         : ||| |    : ||  :
Db        335 VFFSVLIGAFSIGQASPSIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIKGNLE 394

Qy         60 -----FSY----------------TGQTAALYNQAGC 75
                   |||                :||| ||   :||
Db        395 FKNVHFSYPSRKEVKILKGLNLKVQSGQTVALVGNSGC 432
```

RESULT 10
US-09-672-725C-4
; Sequence 4, Application US/09672725C
; Patent No. 6753177
; GENERAL INFORMATION:
; APPLICANT: Stocker, Penny J.
; APPLICANT: Steimel-Crespi, Dorothy T.
; APPLICANT: Crespi, Charles L.
; APPLICANT: Rief, Timothy C
; APPLICANT: Patten, Christopher J.
; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
; FILE REFERENCE: G0307/7017
; CURRENT APPLICATION NUMBER: US/09/672,725C
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/156,510
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-672-725C-4

Query Match 12.5%; Score 69; DB 4; Length 1280;
Best Local Similarity 25.5%; Pred. No. 32;
Matches 25; Conservative 12; Mismatches 33; Indels 28; Gaps 3;

```
Qy          6 LFFSVITVMMLIAMASEMV------NGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYD 59
              :||||:     |  ||  :       |:|: ::         : ||| |    : ||  :
Db        335 VFFSVLIGAFSIGQASPSIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIKGNLE 394

Qy         60 -----FSY----------------TGQTAALYNQAGC 75
                   |||                :||| ||   :||
Db        395 FKNVHFSYPSRKEVKILKGLNLKVQSGQTVALVGNSGC 432
```

RESULT 11
US-10-044-671-2
; Sequence 2, Application US/10044671
; Patent No. 6790621
; GENERAL INFORMATION:
; APPLICANT: Washington State University Research Foundation
; APPLICANT: Mealey, Katrina
; APPLICANT: Bentjen, Steven
; TITLE OF INVENTION: MDR1 VARIANTS AND METHODS FOR THEIR USE
; FILE REFERENCE: 4630-61733
; CURRENT APPLICATION NUMBER: US/10/044,671
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/261,578
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/314,829
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-044-671-2

Query Match 12.5%; Score 69; DB 4; Length 1280;
Best Local Similarity 25.5%; Pred. No. 32;
Matches 25; Conservative 12; Mismatches 33; Indels 28; Gaps 3;

```
Qy          6 LFFSVITVMMLIAMASEMV------NGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYD 59
              :||||:     |  ||  :       |:|: ::         : ||| |    : ||  :
Db        335 VFFSVLIGAFSIGQASPSIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIKGNLE 394

Qy         60 -----FSY----------------TGQTAALYNQAGC 75
                   |||                :||| ||   :||
Db        395 FKNVHFSYPSRKEVKILKGLNLKVQSGQTVALVGNSGC 432
```

RESULT 12
US-09-672-725C-2
; Sequence 2, Application US/09672725C
; Patent No. 6753177
; GENERAL INFORMATION:
; APPLICANT: Stocker, Penny J.
; APPLICANT: Steimel-Crespi, Dorothy T.
; APPLICANT: Crespi, Charles L.
; APPLICANT: Rief, Timothy C
; APPLICANT: Patten, Christopher J.
; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
; FILE REFERENCE: G0307/7017
; CURRENT APPLICATION NUMBER: US/09/672,725C
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/156,510
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1281
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-672-725C-2

Query Match 12.5%; Score 69; DB 4; Length 1281;
Best Local Similarity 25.5%; Pred. No. 32;
Matches 25; Conservative 12; Mismatches 33; Indels 28; Gaps 3;

```
Qy          6 LFFSVITVMMLIAMASEMV------NGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYD 59
              :||||:     |  ||  :       |:|: ::         : ||| |    : ||  :
Db        336 VFFSVLIGAFSIGQASPSIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIKGNLE 395

Qy         60 -----FSY----------------TGQTAALYNQAGC 75
                   |||                :||| ||   :||
Db        396 FKNVHFSYPSRKEVKILKGLNLKVQSGQTVALVGNSGC 433
```

RESULT 13
US-09-672-725C-23
; Sequence 23, Application US/09672725C
; Patent No. 6753177
; GENERAL INFORMATION:
; APPLICANT: Stocker, Penny J.
; APPLICANT: Steimel-Crespi, Dorothy T.
; APPLICANT: Crespi, Charles L.
; APPLICANT: Rief, Timothy C
; APPLICANT: Patten, Christopher J.
; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
; FILE REFERENCE: G0307/7017
; CURRENT APPLICATION NUMBER: US/09/672,725C
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/156,510
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 1281

; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-672-725C-23

Query Match 12.5%; Score 69; DB 4; Length 1281;
Best Local Similarity 25.5%; Pred. No. 32;
Matches 25; Conservative 12; Mismatches 33; Indels 28; Gaps 3;

```
Qy          6 LFFSVITVMMLIAMASEMV------NGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYD 59
              :||||:     |  ||  :      |:|: ::        : ||| |    : ||  :
Db        336 VFFSVLIGAFSIGQASPSIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIKGNLE 395

Qy         60 -----FSY----------------TGQTAALYNQAGC 75
                   |||                :||| ||   :||
Db        396 FKNVHFSYPSRKEVKILKGLNLKVQSGQTVALVGNSGC 433
```

RESULT 14
US-09-672-725C-25
; Sequence 25, Application US/09672725C
; Patent No. 6753177
; GENERAL INFORMATION:
; APPLICANT: Stocker, Penny J.
; APPLICANT: Steimel-Crespi, Dorothy T.
; APPLICANT: Crespi, Charles L.
; APPLICANT: Rief, Timothy C
; APPLICANT: Patten, Christopher J.
; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
; FILE REFERENCE: G0307/7017
; CURRENT APPLICATION NUMBER: US/09/672,725C
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/156,510
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 1281
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-672-725C-25

Query Match 12.5%; Score 69; DB 4; Length 1281;
Best Local Similarity 25.5%; Pred. No. 32;
Matches 25; Conservative 12; Mismatches 33; Indels 28; Gaps 3;

```
Qy          6 LFFSVITVMMLIAMASEMV------NGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYD 59
              :||||:     |  ||  :      |:|: ::        : ||| |    : ||  :
Db        336 VFFSVLIGAFSIGQASPSIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIKGNLE 395

Qy         60 -----FSY----------------TGQTAALYNQAGC 75
                   |||                :||| ||   :||
Db        396 FKNVHFSYPSRKEVKILKGLNLKVQSGQTVALVGNSGC 433
```

RESULT 15
US-09-672-725C-27
; Sequence 27, Application US/09672725C
; Patent No. 6753177
; GENERAL INFORMATION:
; APPLICANT: Stocker, Penny J.
; APPLICANT: Steimel-Crespi, Dorothy T.
; APPLICANT: Crespi, Charles L.
; APPLICANT: Rief, Timothy C
; APPLICANT: Patten, Christopher J.
; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
; FILE REFERENCE: G0307/7017
; CURRENT APPLICATION NUMBER: US/09/672,725C
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/156,510
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 1281
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-672-725C-27

Query Match 12.5%; Score 69; DB 4; Length 1281;
Best Local Similarity 25.5%; Pred. No. 32;
Matches 25; Conservative 12; Mismatches 33; Indels 28; Gaps 3;

```
Qy          6 LFFSVITVMMLIAMASEMV------NGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYD 59
              :||||:     |  ||  :      |:|: ::        : ||| |    : ||  :
Db        336 VFFSVLIGAFSIGQASPSIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIKGNLE 395

Qy         60 -----FSY----------------TGQTAALYNQAGC 75
                   |||                :||| ||   :||
Db        396 FKNVHFSYPSRKEVKILKGLNLKVQSGQTVALVGNSGC 433
```

Search completed: November 5, 2004, 21:56:30
Job time : 45 secs